US-08-713-928A-5.rge

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

3 19:21:38 1998; MasPar time 568.41 Seconds 1157.009 Million cell updates/sec not generated. Tue Feb abular output

1 CAATACGATATTACCGAATA.........CCGGTGAAAGTAAGCAGSTC 463 (1-463) from USO8713928A.seq >US-08-713-928A-5 Description: Perfect Score: Sequence:

GTTATGCTATAATGGCTTAT........GGCCACTTTCATTCGTCWAG

TABLE default Gap 6 Scoring table:

430261 seqs, 710217276 bases x Searched:

Dbase 0; Query 0

STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-new7 Database:

1:BCT 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG3 7:HTG4 8:HUM1 9:HUM2 10:HUM3 11:INV1 12:INV2 13:ORG 14:MAM 15:VRT 16:PLN 17:PRO1 18:PRO2 19:ROD 20:SYN 21:UNC 22:VIR genbanka101 Database

33.8CT1 24.8CT2 25.8CT3 26.8CT4 27.8CT5 28.8CT6 29.8CT7 23.8CT11 33.8CT11 34.8CT2 35.8CT13 33.8CT11 34.8CT12 35.8CT13 35.8CT13 35.6CM1 37.6CBV2 38.6CM3 39.6CBM4 40.6CBV5 41.6CM5 41.6CM6 41.6CM6 41.8CM5 50.1CM7 50.1

genbankb101

Database:

115:VRL1 116:VRL2 117:VRL3 118:VRL4 119:VRL5 120:VRL6 121:VRL7 122:VRL8 123:VRL9 124:VRL10 125:VRL11 126:BCT 127:GEN 128:HTG1 129:HTG2 130:INV 131:MAM 132:VRT 133:PHG 134:PLN1 135:PLN2 136:PRI1 137:PRI2 138:ROD 139:SXN 140:UNA 141:VRL genbank-new7

Database:

Database:

Variance 9.088; scale 1.204 142:part1 143:part2 Mean 10.942; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

[1] 1-16720

and is derived by analysis of the total score distribution.

SUMMARIES

LEUGRO72 Lycopersicon esculent 1.91e-1. LEUGRO73 Lycopersicon esculent 1.91e-1. LEUGRO73 Lycopersicon complete 2.68e-0. LEUGRO73 Lycopersicon esculent 1.91e-1. LEUGRO73 Lycopersicon esculent 1.91e-1. LEUGRO71 Lycopersicon esculent 3.24e+0. Lyco								
28 92.4 16720 16 LEUG68072 Lycopersicon esculent 191e-194 65.5 2884 84 COMPAGED Lycopersicon esculent 191e-194 18.5 2884 84 COMPAGED Lycopersicon esculent 191e-195 7.5 18.5 18.5 18.5 18.5 18.5 18.5 18.5 18	Š	ore	Query Match		DB	۵	Description	δ.
92.4 16720 134 IEUG8072 İycopersicon esculent 1:91e-19 93.5 184 84 TOMHMGZA TOMHGGA 3 Hydroxy3-me 2:35e-126 93.7 184 78 EBUG8072 TOMHGGA 3 Hydroxy3-me 2:35e-126 93.7 184 78 EBUG8072 TOMHGGA 1:55e-126 93.7 184 78 EBUG8073 TOMHGGA 2:05e-02 93.7 1909 76 DDGCP806 D.discoideum discoid 2:02e-02 93.7 1124 39 DDGCP806 D.discoideum culminat 6:22e-01 93.6 12379 51 DD31 P.CAPLED CALCHARD CALCHARD CALCHARD 1:43e-00 93.6 122 134 EBUG8071 CALCHARD RESCOIDENCING IN PRO 1:43e-00 93.6 192 134 EBUG8071 LYCOPERSICON ESCULENT 3:24e-00 94.6 192 134 EBUG8071 LYCOPERSICON ESCULENT 3:24e-00 95.8 192 134 EBUG8071 LYCOPERSICON ESCULENT 3:24e-00 95.8 192 134 EBUG8071 LYCOPERSICON ESCULENT 3:24e-00 96.5 192 134 EBUG8071 LYCOPERSICON ESCULENT 3:26e-00 96.5 192 134 EBUG8071 LYCOPERSICON ESCULENT 3:26e-00 97 17 197 18 EBUG807 LYCOPERSICON ESCULENT 3:26e-00 97 17 17 17 17 17 17 17 17 17 17 17 17 17	i .	428		16720		: 2	esculen	.91e-19
94 63.5 2884 84 TOMHMG2A Tomate 3.hydroxy-3-me 2.35e-12 7.8 1095 76 DDICSON		428	ζ.	16720	13	0	escule	.91e-19
184 78 LEU66072 Lycopersicon esculent 1 1 1095 76 DDICSA Dictyostellum discoid 2 3 3 3 5 DDI		294	ო	2884		TOMHMG2A	-yxc	.35e-12
7.8 1095 76 DDICSA Dictyostelium discoid 2 7.8 3700 51 DDGF80G D.discoideum gobo gen 2 7.1 14001 57 PFCOMPIRB P.falciparum complete 5 5 1124 39 51 DD314 F2589-T7.2 IGF Azabid 1 6 7 1824 39 1812074 F2589-T7.2 IGF Azabid 1 6 7 1824 39 1812074 F2589-T7.2 IGF Azabid 1 6 7 1824 39 EERONTS S.douglasii gene for 1 6 7 50751 42 CEROJH6 *** SEQUENCING IN PRO 1 192 18 LEUG8071 Lycopersicon esculent 3 192 18 LEUG8071 Lycopersicon esculent 3 6 5 186 125 VSVGIYPO Vesicular stomatitis 6 5 186 125 VSVGIYPO Vesicular stomatitis 7 PLOGOF 1 10 10 10 10 10 10 10 10 10 10 10 10 1		156	ო	184		~		.58e-5
7.8 3700 51 DDGP80G D.discoideum gp80 gen 2. 7.1 1400157 PFCOMPIRB P. Falciparum complete 5. 9 2379 51 DD31 PC0MPIRB P. Falciparum complete 5. 6.7 110439 51 DD31 PC045054Ellum discoid 1. 1891 51 DD073685 Dictyostellum discoid 1. 6.7 1891 51 DD073685 Dictyostellum discoid 1. 6.7 1617 78 MISDOCTB S.douglasi gene for 1. 50751 42 CEF02146 *** SEQUENCING IN PRO 1. 6.7 11062 46 HSAC00123 *** SEQUENCING IN PRO 1. 6.5 192 78 LEU68071 Lycopersicon esculent 3. 6.5 192 78 LEU68071 Lycopersicon esculent 3. 6.5 192 78 MITGTRN6 TOTULOPSIS glabrata m 3. 6.5 1868 125 VSVGLYPQ Vesicular stomatitis 6.5 1868 125 VSVGLYPQ Vesicular stomatitis 6.5 3007 57 DD1GP24 D.discoideum glycopro 7. 6.3 3007 57 PFCMDRI P. Falciparum pene for 7. 6.3 3007 77 PFCMDRI P. Falciparum pene for 7. 6.3 3739 94 HSU23302 D.discoideum glycopro 7. 6.3 3739 94 HSU23322 Human DNA sequence fr 7. 6.3 172533 8 HSAC2381 Human DNA sequence fr 7. 6.3 172533 8 HSAC2381 Human DNA sequence fr 7. 6.3 172533 8 HSAC2381 Human DNA sequence fr 6.0 1147 39 B13042 T30M24-Sp6.1 TAMU Arabido 1. 6.0 12895 192 HSLIGALOR Human DNA sequence fr 6.0 12895 192 HSLIGALOR Human DNA sequence fr 6.0 12895 192 HSLIGALOR Human DNA sequence fr 6.0 1952 54 HSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		36		1095		DDICSA	n disc	.02e-0
7.1 14001 57 PFCOMPIRB P. falciparum complete 2 6.9 2379 51 DD31 6.7 11821 39 B12074 6.7 11821 51 DD075885 Dictyostelium discoid 1 6.7 6615 78 EKRO1012 *** SEQUENCING IN PRO 1 6.7 36238 43 CEFCO161 *** SEQUENCING IN PRO 1 6.7 50751 42 CEFCO166 *** SEQUENCING IN PRO 1 6.7 11062 46 HSACOO1237 *** SEQUENCING IN PRO 1 6.5 192 16 LEUG8071 Lycopersicon esculent 3 6.5 864 78 MIGGRAG *** SEQUENCING IN PRO 1 6.5 864 78 MIGGRAG *** SEQUENCING IN PRO 1 6.5 864 87 PLUSSON Lycopersicon esculent 3 6.5 865 57 PLUSSON FORMARION Yeast (T.glabrata) mi 3 6.5 865 57 PLUSSON Yeast (T.glabrata) mi 3 6.5 866 57 PLUSSON Yeast (T.glabrata) mi 3 6.5 866 57 PLUSSON PROSTON YEASTON ALIMATA 16 6.5 33010 50 CELZC196 PARASTONA LIMATA 16 6.5 3000 77 DDIGP24 D.discoideum glycopro 7 6.3 3075 58 KPFRNRPOL P. falciparum gene for 7 6.3 3075 58 KPFRNRPOL P. falciparum gene for 7 6.3 15421 57 PFCOMPIRA P. falciparum gene for 7 6.3 22243 57 PFCOMPIRA P. falciparum gene for 7 6.3 2243 57 PFRONRIA P. falciparum gene for 7 6.3 2243 57 PFRONRIA P. falciparum pene for 7 6.3 2633 57 PFRONRIA P. falciparum pene for 7 6.3 2634 57 PFRONRIA P. falciparum pene for 7 6.3 2644 57 PFRONRIA P. falciparum pene for 7 6.3 17233 94 HSU213G2 Human DNA sequence fr 7 6.3 20043 45 HSU312G2 Human DNA sequence fr 7 6.3 20139 45 HSU312A Human DNA sequence fr 6 6.0 1472 39 HSU60NA POLICA INIT 1 6.0 147 39 B13042 TOR ACADON CONDICTED 1 6.0 147 39 B13042 Human DNA sequence fr 6 6.0 1452 59 HSU613108 Human DNA sequence fr 6 6.0 1452 59 HSU613108 Human DNA sequence fr 6 6.0 1452 59 HSU613108 Human DNA sequence fr 6 6.0 1452 59 HSU613108 Human DNA sequence fr 6 6.0 1452 59 HSU613108 Human DNA sequence fr 6 6.0 1452 59 HSU613108 Human DNA sequence fr 6 6.0 1452 59 HSU613108 Human DNA sequence fr 6 6.0 1969 51 HUMAN DNA SEQUENCE FI 1 6.0 1960 51 DDECNA DOTAPADIGITIS elegan 1 6.		36		3700		DDGP80G	9980	.02e-0
6.9 2379 51 DD314 D.discoideum culminat 6 6.7 1824 39 B12074 F2589-T7.2 IGF Arabid 11 6.7 18218 43 CEKOIG12 *** SEQUENCING IN PRO 15 6.7 50751 42 CEKOIG12 *** SEQUENCING IN PRO 15 6.5 1922 6 HSAC001237 *** SEQUENCING IN PRO 15 6.5 1922 16 LEUGRO71 LYCOPERSICON esculent 3 6.5 192 16 LEUGRO71 LYCOPERSICON esculent 3 6.5 854 78 MITGTRN6 TOTULOPSIS Glabrata m 3 6.5 854 78 MITGTRN6 TOTULOPSIS Glabrata m 3 6.5 865 57 PLU39369 Vesicular stomatitis 6 6.3 33010 50 CELZC196 Caenorhabditis elegan 3 6.3 3000 77 DDIGP24 D.discoideum glycopro 7 6.3 3000 77 DDIGP24 D.discoideum glycopro 7 6.3 3005 58 PEPRWDR1 P. Falciparum Gene for 7 6.3 3075 58 XPERNAPOL P. Falciparum Gene for 7 6.3 3739 54 HSU23302 Human DNA Sequence fr 7 6.3 172533 8 HSAC2381 Human DNA Sequence ** 7 6.3 172533 8 HSAC2381 Human DNA Sequence ** 7 6.3 172533 8 HSAC2381 Human DNA Sequence ** 7 6.3 172533 8 HSAC2381 Human DNA Sequence ** 7 6.3 172533 8 HSAC2381 Human DNA Sequence ** 7 6.0 1452 55 HSU63108 Human DNA Sequence ** 7 6.1 147 39 B13042 730MA-Sp6. 1AMU Arabido 1 6.0 1452 55 HSU63108 Human Complete 6 6.0 1462 55 HSU63108 Human Complete 6 6.0 17084 6 DVMTGNME D.Virginiana complete 6 6.0 28951 92 HSU6713 Caenorhabditis elegan 1 6.0 28951 92 HSU6713 CAENORYA CA		33		14001		MPI	compl	.68e-0
6.7 1124 39 B12074 F25H9-T7.2 IGF Arabid 1. 66.7 1891 51 DDU73685 Dictyostellum discoid 1. 66.7 36238 43 CEK01G12 *** SEQUENCING IN PRO 1. 50.751 42 CEF02H6 *** SEQUENCING IN PRO 1. 192 16 LEU68071 Lycopersicon esculent 3. 192 18 LEU68071 Lycopersicon esculent 3. 6.5 192 78 LEU68071 Lycopersicon esculent 3. 6.5 192 78 LEU68071 Lycopersicon esculent 3. 6.5 192 78 MITGTRN6 Teast (T.glabrata) mi 3. 6.5 864 85 YSLMTG08 Yeast (T.glabrata) mi 3. 6.5 865 57 PLU33969 Vesicular stomatitis 3. 6.5 33010 50 CEL2C196 Caenorhabditis elegan 3. 6.3 8739 94 Parastenopa limata 16. 8. 868 125 VSVGLYPQ Caenorhabditis elegan 3. 6.3 863 57 PEPEMDRI Praspiens (haplotype 7. 6.3 876 39 B12885 Dissmodium falciparum omplete 7. 6.3 8739 94 HSU23322 Human DNA sequence fr 7. 8. 863 57 PEPEMDRI Praspiens practical growth of 3. 863 57 PEPEMDRI Praspiens findling falciparum omplete 7. 6.3 17253 8 HSAC2381 Human DNA sequence fr 7. 8. 95936 44 HS12714 Human DNA sequence fr 7. 8. 317533 8 HSAC2381 Human DNA sequence fr 6.3 20034 45 HS415G2 Human DNA sequence fr 6.3 20139 45 HS415G2 Human DNA sequence fr 6.0 147 39 B13042 T30M24-Sp6 1 TAMU Arabido 1. 145 25 HS66 50 DVMTGNME DVISIONAR EDUCACHE 1. 10 10 10 10 10 10 10 10 10 10 10 10 10		32		2379		DD31	D.discoideum culminat	.22e-0
6.7 1891 51 DD075685 Dictyostelium discoid 1. 6615 78 MISDCYTB 8.4 SEQUENCING IN PRO 1. 5.7 36238 43 CEROJGG 8.4.4 SEQUENCING IN PRO 1. 5.7 11062 46 HSACO10127 *** SEQUENCING IN PRO 1. 5.9 11062 46 HSACO10127 *** SEQUENCING IN PRO 1. 5.9 192 16 LEUG8071 Lycopersicon esculent 3. 192 78 LEUG8071 Lycopersicon esculent 3. 5.9 78 4 78 MITGTRN6 Feast (T.glabrata) mi 3. 6.5 864 85 YSLMTIGO8 Yeast (T.glabrata) mi 3. 6.5 865 17 PL039569 Parastenopa limata 16 3. 116 66 A08900 H. sapiens (haplotype 6.3 3000 77 DDIGP24 D.discoideum glycopro 7. 6.3 3000 77 DDIGP24 D.discoideum glycopro 7. 6.3 3000 77 DDIGP24 D.discoideum glycopro 7. 6.3 863 57 PFCOMPIRA P. Falciparum gene for 7. 6.3 15421 57 PFCOMPIRA P. falciparum gene for 7. 6.3 2243 57 PFCOMPIRA P. falciparum pene for 7. 6.3 2243 57 PFCOMPIRA P. falciparum pene for 7. 6.3 2243 57 PFCOMPIRA P. falciparum falciparum 7. 6.3 2243 57 PFCOMPIRA P. falciparum complete 7. 6.3 2243 57 PFCOMPIRA P. falciparum falciparum 7. 6.3 2243 57 PFCOMPIRA P. fal		31	•	1124		B12074	F25H9-T7.2 IGF Arabid	.43e+0
6.7 6615 78 MISDCYTB S.douglasii gene for 1 5.7 36238 43 CEKOLO12 *** SEQUENCING IN PRO 1 192 16 LEUGRO71 LYCOPERSICON esculent 3 6.5 192 16 LEUGRO71 LYCOPERSICON esculent 3 6.5 192 18 LEUGRO71 LYCOPERSICON esculent 3 6.5 854 78 MITGTRN6 TOTULOPSIS glabrata m 3 6.5 854 78 MITGTRN6 TOTULOPSIS glabrata m 3 6.5 865 57 PLU39369 Vesicular stomatitis 6.5 33010 50 CELZC196 Cemorrhadditis elegan 3 6.3 3000 77 DDIGP24 D.discoideum glycopro 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		31		1891		DDU73685	Dictyostelium discoid	43e+0
6.7 36238 43 CEKOIG12 *** SEQUENCING IN PRO 15.7 11062 46 HSACO01237 *** SEQUENCING IN PRO 15.7 11062 46 HSACO01237 *** SEQUENCING IN PRO 15.9 192 16 LEU68071 Lycopersicon esculent 3.6.5 192 78 LEU68071 Lycopersicon esculent 3.6.5 854 78 MITGTRN6 Feast (T.glabrata) mi 3.6.5 865 57 PLU39369 Feast (T.glabrata) mi 3.6.5 1868 125 VSVGLYPQ Vesicular stomatifis 3.3010 50 CEL2C196 Caenorhabditis elegan 3.16 6.3 876 39 B12885 Discoldeum glycopro 7.0 1863 57 PERMAPOL PISACOIDEUM falciparum formplete 7.0 1863 57 PERMAPOL PISACOIDEUM falciparum complete 7.0 1863 57 PERMAPOL PISACOIDEUM falciparum falciparum 6.3 2243 57 PERMAPOL PISACOIDEUM falciparum 6.3 2243 57 PERMAPOL PISACOIDEUM falciparum 6.3 20043 45 HS12124 Human DNA sequence fr 7.0 1860 51 1860 5		31		6615		MISDCYTB	ane.	436+
6.7 50751 42 CEF02H6 *** SEQUENCING IN PRO 11062 46 HSAC001237 *** SEQUENCING IN PRO 15. 192 16 LEUG8071 Lycopersicon esculent 3. 192 78 LEUG8071 Lycopersicon esculent 3. 192 78 LEUG8071 Lycopersicon esculent 3. 5. 864 78 MITGTRN6 Feast (T.glabrata) mi 3. 6.5 1865 17 PLU39569 Parastenopa limata 16 3. 1868 125 VSVGLYPQ Caenorhabditis elegan 3. 116 60 A08900 H.sapiens (haplotype 7. 87 2007 77 DDIGP24 D.discoideum glycopro 7. 87 2007 77 DDIGP24 D.discoideum glycopro 7. 87 2007 77 PFCOMPIRA P. Falciparum gene for 7. 6.3 3075 58 XPFRNAPOL P. falciparum gene for 7. 6.3 7038 57 PFCOMPIRA P. falciparum gene for 7. 6.3 15421 57 PFCOMPIRA P. falciparum gene for 7. 6.3 22243 57 PFCOMPIRA P. falciparum pene for 7. 6.3 2243 57 PFCOMPIRA P. falciparum complete 7. 6.3 2243 57 PFCOMPIRA P. falciparum formoliti S. 3 20043 4 HSU213G2 Human DNA sequence fr 7. 6.3 20043 45 HSU312G2 Human DNA sequence fr 6.3 20043 45 HSU312G1 Human DNA sequence ** 7. 6.0 1147 39 B13042 T30M24-Sp6.1 TAMU Ara 16.0 1950 51 DDECMA D.discoideum ecmA pro 6.0 1147 39 B13042 T30M24-Sp6.1 TAMU Ara 16.0 1950 51 DDECMA D.discoideum ecmA pro 6.0 2019 84 STU5198 Solanum tuberosum Clo 16.0 2895192 HSU6173 Caenorhabditis elegan 1. 6.0 2895192 HSU3139 CAENOR		31	٠,	36238		CEK01G12	SECUENCING IN	4364
6.7 111062 46 HSACO01237 *** SEQUENCING IN PRO 1 192 16 LEU68071 Lycopersicon esculent 3 6.5 192 13 LEU68071 Lycopersicon esculent 3 6.5 854 78 MITGTRN6 Torulopsis glabrata m 3 6.5 865 57 PLU39569 Vestcular stomatitis 5 86 57 PLU39569 Vesicular stomatitis 3 6.5 33010 50 CELZC196 Cemorrhadditis elegan 3 6.3 3000 77 DDIGP24 D. discoideum glycopro 7 DDIGP24 D. discoideum falciparum 6.3 3075 58 XPFRMDRI P. falciparum pfmdri g 7 DFCP1553 PFPAMRRAD P. falciparum pfmdri g 7 DFCP1573 PFPAMRAD P. falciparum pfmdri g 7 DFCP1573 PFPAMRAD P. falciparum pfmdri g 7 DFCP1574 Human DNA sequence ** 7 DFCP1573 B HSAC2381 Human DNA sequence ** 7 DFCP1574 Human DNA Sequen		31	٠,	50751		110	SECTIENCING IN	430
6.5 192 16 EBU68071 Lycopersicon esculent 3. 192 18 LEU68071 Lycopersicon esculent 3. 192 134 MITGTRN6 Feast (T.qlabrata) mi 3. 6.5 854 85 YSLWTIGOB Yeast (T.qlabrata) mi 3. 6.5 865 85 YSLWTIGOB Yeast (T.qlabrata) mi 3. 6.5 1868 125 YSVGIPPO Vesicular stomatitis 3. 1868 125 YSVGIPPO Vesicular stomatitis 3. 186 3. 18		31		111062		123	SECIENCING IN	4364
6.5 192 78 LEU68071 Lycopersicon esculent 5 6.5 854 78 MITGTRN6 Torulopsis glabrate m 3 6.5 854 78 MITGTRN6 Teast (T.glabrata) mi 5 6.5 865 57 PLU39369 Parastenopa limata 16 3 6.5 1868 125 VSVGIYPO Vesicular stomathis 3 6.5 33010 50 CELCC196 H.saphens (Implorype 6.3 3000 77 DDIGP24 D.discoideum glycopro 7 DDIGP24 D.discoideum complete 6.3 17253 B.HSAC3381 Human DNA sequence ** 7 DDIGP24 D.discoideum ecmA pro 1 DDECMA SOLOTABOLISE ELEGAN 1 D.discoideum ecmA pro 1 DDECMA D.dispinana complete 1 DDECMA D.dispinana complete 1 DDIGPS D.Virginiana complete 1 DDIGPS D.Virginiana complete 1 DDIGPS D.DIGPS D.DIG		10		201		; -	Opere i con secui	1000
192 134 EDG68071 Lycopersicon esculent 3: 6.5 854 78 MITGTRN6 Torulopsis glabrata m 3: 6.5 864 57 PLU39569 Vestcular stomatitis 3: 6.5 865 57 PLU39569 Vestcular stomatitis 3: 6.5 33010 50 CELZC196 Caenorhabditis elegan 3: 6.3 33010 50 CELZC196 Caenorhabditis elegan 3: 6.3 3000 77 DDIGE24 D.discoideum glycopro 7: 6.3 3005 58 XPFRNAPOL P.falciparum gene for 7: 7000 77 DDIGE24 D.discoideum glycopro 7: 6.3 3000 77 PFPWDR1 P.falciparum gene for 7: 7000 78 57 PFPWDR1 P.falciparum gene for 7: 7000 78 70 PFPWDR1 P.falciparum pfmdr1 g 7: 7000 78 70 PFPWDR1 P.falciparum pfmdr1 g 7: 70 PFPWDR1 P.falciparum pfmdr2 g 7: 70 PFPWDR1 P.falciparum pfm		0 0		100		1 500000	Though the	1047
197 194 195 LEUROBOVI L'ACOPPETSION SCALLIERT S' 196 178 MITGERNG Reast (T.glabrata) mi 3 6.5 865 77 PLUSD9569 Parastenopa limata 16 3 6.5 1865 17 PLUSD959 Parastenopa limata 16 3 6.5 1865 17 PLUSD969 Parastenopa limata 16 3 6.5 33010 50 CELZC196 Vestquars stomatitis elegan 3 116 66 A08900 H.saplens (haplotype 7 178 3 178 59 RYPENBRAPOL P.falciparum gene for 7 178 18 18 18 18 18 18 18 18 18 18 18 18 18		0 0	٠	7 6	0 (100001	escare	٠,
6.5 854 78 MITGTRN6 ToruLopsis glabrata m 3. 6.5 865 57 PLU39369 Parastenopal limata 6.5 865 57 PLU39369 Parastenopal limata 6.5 865 57 PLU39369 Parastenopal limata 6.5 33010 50 CELZC196 Caenorhabditis elegan 3. 6.3 3300 77 DDIGEP24 Delisorideum glaplotype 6.3 3000 77 DDIGEP24 Delisorideum glapotype 6.3 3000 77 PFCRNAPOL P.falciparum gene for 7. 6.3 7038 57 PFCRNAPOL P.falciparum gene for 7. 6.3 1542157 PFCOMPIRA P.falciparum gene for 7. 6.3 1542157 PFCOMPIRA P.falciparum falciparum 7. 6.3 1542157 PFCOMPIRA P.falciparum falciparum 7. 6.3 1542157 PFCOMPIRA P.falciparum falciparum 7. 6.3 1543157 PFCOMPIRA P.falciparum falciparum 7. 6.3 1543157 PFCOMPIRA P.falciparum falciparum 7. 6.3 172533 64 HS12774 Human DNA sequence ** 7. 6.3 172533 8 HSAC3381 Human DNA sequence ** 7. 6.3 172533 8 HSAC3381 Human DNA sequence ** 7. 6.0 147239 45 HS43501 Human DNA sequence ** 7. 6.0 1452 94 5 HS43501 F19A23-77 IGF Arabido 1. 6.0 1473 94 STUG198 50 D.virginiana complete 1. 6.0 17084 60 DVMTGNME D.virginiana complete 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence ** 7. 6.0 28951 92 HSLIGAC3 Human DNA sequence ** 7. 6.0 28951 92 HSLIGAC3 Human DNA sequence ** 7. 6.0 1452 95 HSUG3108 Human eukaryotic init 1. 6.0 1482 95 HSUG3108 Human eukaryotic init 1. 6.0 1462 95 HSUG3108 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 Human DNA sequence fr 1. 6.0 28951 92 HSLIGAC3 HUMAN SEQUENCE FI 1. 6.0 28951 92 HSLIGAC3 HUMAN DNA SEQUENCE FI 1. 6.0 28951 92 HSLIGAC3 HAMAN DNA SEQUENCE FI 1. 6.0 28951 92 HSLIGAC3 HAMAN DNA SEQUENCE FI		2 0		77.	3	7/08077	con escut	٠. س
6.5 864 85 YSLWTICOB Yeast (T.glabrata) mi 3. 6.5 1868 125 VSVGIPPO 6.5 1868 125 VSVGIPPO 6.5 1868 125 VSVGIPPO 6.5 1868 125 VSVGIPPO 6.3 3010 50 CELZC196 Caenorhabditis elegan 3. 6.3 876 39 B12885 T17AB-T7 RAWD Arabido 6.3 3007 77 DDIGP24 D.discoideum glycopro 6.3 3075 58 XPFRNAROL P.falciparum gene for 7. 6.3 18633 57 PFFRNDRIA P.falciparum complete 7. 6.3 15421 57 PFCOMPIRA P.falciparum complete 7. 6.3 18421 57 PFCOMPIRA P.falciparum complete 7. 6.3 22443 57 PFCOMPIRA P.falciparum complete 7. 6.3 2243 57 PFCOMPIRA P.falciparum complete 7. 6.3 2243 57 PFCOMPIRA P.falciparum complete 7. 6.3 2243 57 PFCOMPIRA P.falciparum complete 7. 6.3 28078 48 CEF21R12 Caenorhabditis elegan 7. 6.3 25936 44 HS12714 Human DNA sequence fr 7. 6.3 17239 45 HS12714 Human DNA sequence fr 7. 6.3 20434 45 HS41562 Human DNA sequence ** 7. 6.3 20139 45 HS41561 Human DNA sequence ** 7. 6.0 1147 39 B13042 T30M24-Sp6 1 TAMU Ara 1. 6.0 1452 59 HS063108 Human DNA sequence fr 7. 6.0 1969 61 DDECMA D.discoideum ecmA pro 1. 6.0 17084 60 DVMTGNME D.virginiana complete 1. 6.0 28951 92 HSLIGATA CAENORADILIS elegan 1. 6.0 28951 92 HSLIGATA Human DNA sequence fr 7. 6.0 28951 92 HSLIGATA Human DNA sequence fr 7. 6.0 1968 60 DVMTGNME D.virginiana complete 1. 6.0 28951 92 HSLIGATA Human DNA sequence fr 7. 6.0 28951 92 HSLIGATA Human DNA sequence fr 7. 6.0 28951 92 HSLIGATA Human DNA sequence fr 7. 6.0 28951 92 HSLIGATA Human DNA sequence fr 7. 6.0 28951 92 HSLIGATA Human DNA sequence fr 6.0 17084 60 DVMTGNME D.virginiana complete 1.		30	٠	854			glabrate	2
6.5 865 57 PLU39369 Parastenopa limata 16 3. 6.5 1868 125 VSVGLYPQ Vesicular stomatitis 3 6.5 33010 50 CELECC196 6.3 876 39 B12885 T17AB T7 TAMU Arabido 7. 6.3 3000 77 DDIGP24 D. discoideum glycopro 7. 6.3 3005 58 XPERNAPOL P. falciparum gene for 7. 6.3 1038 57 PFPENDRA P. falciparum gene for 7. 6.3 1541 57 PFPENDRA P. falciparum gene for 7. 6.3 1542 157 PFPENDRA P. falciparum gene for 7. 6.3 1542 157 PFPENDRA P. falciparum gene for 7. 6.3 1542 157 PFPENDRA P. falciparum falciparum 7. 6.3 1543 57 PFPENDRA P. falciparum falciparum 7. 6.3 1543 57 PFPENDRA P. falciparum falciparum 7. 6.3 3739 94 HSU2023G2 Human DNA sequence ** 7. 6.3 200434 45 HS415G2 Human DNA sequence ** 7. 6.3 17253 8 HSAC2381 Human DNA Sequence ** 7. 6.3 201239 45 HS415G2 Human DNA Sequence ** 7. 6.0 147 39 B13042 T300A2 Seb. 1 TAMU Ara 1. 6.0 1462 95 HSU61108 Human eukaryotic init 6.0 1462 95 HSU61108 Human eukaryotic init 6.0 147 39 HSU61108 D. virginiana complete 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1. 6.0 28951 92 HSLIGACA Human DNA Sequence fr 1.		30	٠	854		0	labrata)	24
6.5 1868 125 VSVGLYPQ Vesicular stomatitis 33010 50 CELZC196 Caenorhabditis elegan 3.6.3 33010 50 CELZC196 Caenorhabditis elegan 3.6.3 876 39 B12885 T17A8-T7 TAMU Arabido 7.6.3 3000 77 DDIGP24 Dissocideum glycopro 7.6.3 7038 57 PFCRMPR1 P.falciparum gene for 7.6.3 15421 57 PFCMPIRA P.falciparum falciparum 6.3 2243 57 PFCMPIRA P.falciparum complete 7.6.3 15421 57 PFCMPIRA P.falciparum complete 7.6.3 15421 57 PFCMPIRA P.falciparum complete 7.6.3 2243 57 PFCMPIRA P.falciparum complete 7.6.3 15421 57 PFCMPIRA P.falciparum complete 7.6.3 28078 48 CEF21F12 Caenorhabditis elegan 7.6.3 3739 34 HSU2774 Human DNA sequence 4* 7.6.3 172533 8 HSAC3381 Human DNA sequence 4* 7.6.3 172533 8 HSAC3381 Human DNA sequence 4* 7.6.3 200434 45 HS415G2 Human DNA sequence 4* 7.6.0 1472 39 B13042 T30MA4-Sp6.1 TAMU Ara 1.6.0 1452 95 HSU63108 Human eukaryotic init 1.6.0 19084 60 DVMTGNME D.virginiana complete 1.6.0 28951 92 HSLIGACA Human DNA sequence fr 1.6.0 28951 92 HSLIGACA Human DNA sequence 4* 7.6.0 19084 60 DVMTGNME D.virginiana complete 1.6.0 28951 92 HSLIGACA Human DNA sequence fr 1.6.0 28951 92 HSLIGACA Human DNA sequence fr 1.6.0 28951 92 HSLIGACA Human DNA sequence 4* 7.6.0 19084 60 DVMTGNME D.virginiana complete 1.6.0 28951 92 HSLIGACA Human DNA sequence fr 1.6.0 28951 92 HSLIGACA HUMAN DNA SEQUENCE FI 1		30		865		PLU39369		
6.5 33010 50 CEL2C196 Caenorhabditis elegan 3. 116 66 A08900 H.sapiens (haplotype 7. 6.3 3007 77 DDIGP24 D.discoideum glycopro 7. 6.3 3007 77 DDIGP24 D.discoideum glycopro 7. 6.3 3075 58 XPFRNAPOL P.falciparum gene for 7. 6.3 15421 57 PFCOMDIRA P.falciparum complete 7. 6.3 2243 57 PFCANRTRA P. Falciparum complete 7. 6.3 28078 48 CEF21F12 Caenorhabditis elegan 7. 6.3 28078 48 CEF21F12 Caenorhabditis elegan 7. 6.3 3739 34 HSU2372 Human DNA sequence fr 7. 6.3 17553 8 HSAC2381 Human DNA sequence fr 7. 6.3 10239 45 HSU552 Human DNA sequence ** 7. 6.3 20043 45 HSU552 Human DNA sequence ** 7. 6.0 147 39 B13042 T30M24-Sp6 1 TAMU Ara 1. 6.0 147 39 B13042 T30M24-Sp6 1 TAMU Ara 1. 6.0 1452 59 HSU63108 Human cukaryotic init 1. 6.0 17084 60 DVMTGNME D.virginian complete 1. 6.0 28951 92 HSLIGATS Human DNA sequence fr 6. 6.0 28951 92 HSU63108 Human Cukaryotic init 1. 6.0 28951 92 HSLIGATS Human DNA sequence fr 6. 6.0 28951 92 HSLIGATS Human DNA sequence fr 6. 6.0 28951 92 HSLIGATS Human DNA sequence fr 6. 6.0 28951 92 HSLIGATS Caenorhabditis elegan 1.		30	•	1868	12		ati	ന
6.3 116 66 A08900 H.sapiens (haplotype 7.26 6.3 3000 70 DDIGP24 D.discoideum glycopto 7.26 6.3 3000 70 DDIGP24 D.discoideum glycopto 7.26 6.3 3075 58 XPFRNAPOL P.falciparum gene for 7.26 6.3 7038 57 PFGP195A Plasmodlum falciparum 7.26 6.3 15421 57 PFCMPTRA P.falciparum complete 7.26 6.3 22243 57 PFCMPTRA P.falciparum complete 7.26 6.3 22043 57 PFAVAR23A Plasmodlum falciparum 7.26 6.3 3739 34 HSU233G2 Human DNA sequence ** 7.26 6.3 3739 34 HSU233G2 Human DNA sequence ** 7.26 6.3 20123 45 HSA35D1 Human DNA sequence ** 7.26 6.3 20123 45 HSA35D1 Human DNA sequence ** 7.26 6.3 20123 45 HSA35D1 PRAAC3 T7 IGF Arabido 1.61 6.0 1147 39 B11004 T30M24-Sp6.1 TAMU Ara 1.61 6.0 1950 51 DDECMA D.discoideum ecumA pro 1.61 6.0 2019 84 STU51985 Solanum tubercoum clo 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence ** 7.26 6.0 1960 51 DDECMA D.virginiana complete 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ Human DNA sequence F. 1.61 6.0 28951 92 HSLIGICZ HUMAN SEQUENCE F.		30		33010	2		Caenorhabditis elegan	•
6.3 876 39 B12885 T17A8-T7 TANU Arabido 7.26 6.3 3000 77 DDIGP24 D.discoideum glycopro 7.26 6.3 3075 SYPFRMAPOL 6.3 1008 57 PFGP195A P.falciparum gene for 7.26 6.3 7038 57 PFGP195A P.falciparum gene for 7.26 6.3 15421 57 PFCOMPIRA P.falciparum pfmdr1 g 7.26 6.3 22243 57 PFCOMPIRA P.falciparum complete 7.26 6.3 22243 57 PFCOMPIRA P.falciparum falciparum 7.26 6.3 3739 94 REF2IF12 Caenorhabditis elegan 7.26 6.3 3739 34 HSU232G2 Human DNA sequence fr 7.26 6.3 3739 34 HSU23C4 Human DNA sequence fr 7.26 6.3 17253 8 HSAC2381 Human DNA sequence ** 7.26 6.3 20123 45 HS455D1 Human DNA sequence ** 7.26 6.0 512 39 B11004 T30M24-Sp6.1 TAMU Ara 1.61 6.0 1452 95 HSU63108 Human eukaryotic init 1.61 6.0 1452 95 HSU65108 Human cenkaryotic init 1.61 6.0 17084 60 DDECMA D.discoideum econA pro 1.61 6.0 2019 84 STU51885 Solanum tuberosum clo 1.61 6.0 28951 92 HSL16173 Caenorhabditis elegan 1.61		53		116	9	A08900	H.sapiens (haplotype	
6.3 3000 77 DDIGP24 D.discoideum glycopro 7.26 6.3 3075 58 XPFRNPPOL P.falciparum gene for 7.26 6.3 7038 57 PFFPUSR1 P.falciparum gene for 7.26 6.3 18633 57 PFFPUSR1 P.falciparum gene for 7.26 6.3 18635 57 PFFPUSR1 P.falciparum pfmdr1 g 7.26 6.3 22243 57 PFFVARZ3A Plasmodium falciparum 7.26 6.3 2284 57 PFFVARZ3A Caenorhabditis elegan 7.26 6.3 28078 48 CEF21F12 Caenorhabditis elegan 7.26 6.3 37393 44 HSU23242 Human DNA sequence fr 7.26 6.3 172533 8 HSAC2381 Human DNA sequence ** 7.26 6.3 20123 45 HS415G2 Human DNA sequence ** 7.26 6.3 20123 45 HS415G2 Human DNA sequence ** 7.26 6.0 1472 95 HSU63108 Human eukaryotic init 1.61 6.0 1452 95 HSU63108 Human eukaryotic init 1.61 6.0 1950 15 DDECMA D.discoideum ecmA pro 1.61 6.0 2019 84 STU5188 Solanum tuberosum clo 1.61 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26 6.0 28951 92 HSL16102 Human DNA sequence fr 7.26		53	٠	876	ᠬ	B12885	T17A8-T7 TAMU Arabido	
6.3 3075 58 XPFRNAPOL P.falciparum gene for 7.26 6.3 8633 57 PFGF195A Plasmodium falciparum 7.26 6.3 15421 57 PFGPNBRA P.falciparum pfmf1 g 7.26 6.3 15421 57 PFCOMPIRA P.falciparum complete 7.26 6.3 22243 57 PFAVARZ3A Plasmodium falciparum 7.26 6.3 37393 94 HSU2322 Human DNA Sequence 7.26 6.3 37393 94 HSU2322 Human DNA Sequence ** 7.26 6.3 200434 45 HSL27L4 Human DNA Sequence ** 7.26 6.3 201239 45 HSL35D1 Human DNA Sequence ** 7.26 6.3 201239 45 HSL35D1 Human DNA Sequence ** 7.26 6.3 201239 45 HSL35D1 Human DNA Sequence ** 7.26 6.0 1147 39 B11004 PSA21-T7 IGF Arabido 1.61 6.0 1147 39 B13042 PSD6.1 TAMO Ara 1.61 6.0 1950 51 DDECMA D.discoideum ecmA pro 1.61 6.0 2019 84 STU51985 Solanum tubersoum clo 1.61 6.0 28951 92 HSL161C2 Human DNA Sequence F. 1.61 6.0 28951 92 HSL161C2 Human DNA Sequence F. 1.61 6.0 28951 92 HSL161C2 Human DNA Sequence F. 1.61 6.0 28951 92 HSL161C2 Human DNA Sequence F. 1.61 6.0 34860 50 CELR173 Cenorhabditis elegan 1.61		53		3000	7	DDIGP24	D.discoideum glycopro	
6.3 7038 57 PFGP195A Plasmodium falciparum 7.26 6.3 8633 57 PFPFMDR1 P. falciparum pfmdr1 g 7.26 6.3 15421 57 PFCOMPIRA P. falciparum pfmdr1 g 7.26 6.3 2243 57 PFROMPIRA P. falciparum pfmdr1 g 7.26 6.3 22043 57 PFROMPIRA P. falciparum complete 7.26 6.3 3739 94 HSU23262 Human DNA sequence ** 7.26 6.3 3739 34 HSU23262 Human DNA sequence ** 7.26 6.3 17253 8 HSAC2381 Human DNA sequence ** 7.26 6.3 20123 45 HSA55D1 Human DNA sequence ** 7.26 6.0 1147 39 B11004 T30M24-Sp6.1 TAMU Ara 1.61 6.0 1950 51 DDECMA D.discoideum ecumA pro 1.61 6.0 1950 51 DDECMA D.discoideum ecumA pro 1.61 6.0 1960 51 SHU6108 D.virginiana complete 1.61 6.0 2019 84 STU51885 Solanum tuberosum clo 1.61 6.0 28951 92 HSL16102 Human DNA sequence fr 1.61 6.0 28951 92 HSL16102 Human DNA sequence fr 1.61 6.0 28951 92 HSL16102 Human DNA sequence fr 1.61 6.0 28951 92 HSL16102 Human DNA sequence fr 1.61 6.0 28951 92 HSL16102 Human DNA sequence fr 1.61 6.0 28951 92 HSL16102 Human DNA sequence fr 1.61		53	٠	3075	S	XPFRNAPOL	P.falciparum gene for	. 26
6.3 8633 57 PFPFMDR1 P.falciparum pfmdr1 g 7.26e+ 6.3 15421 57 PFCOMPIRA P.falciparum complete 7.26e+ 6.3 2243 57 PFRANK23A Caenorhabditis elegan 7.26e+ 6.3 228078 48 CEF21F12 Caenorhabditis elegan 7.26e+ 6.3 3739 34 HSU232G2 Human DNA sequence # 7.26e+ 6.3 172533 8 HSAC2381 Human DNA sequence ** 7.26e+ 6.3 20123 45 HS415G2 Human DNA sequence ** 7.26e+ 6.0 147 39 B11004 F19A23-T7 IGF Arabido 1.61e+ 6.0 1442 95 HSU63108 Human eukaryotic init 1.61e+ 6.0 1442 95 HSU63108 Human eukaryotic init 1.61e+ 6.0 2019 84 STU51985 Solanum tuberosum Clo 1.61e+ 6.0 1866 05 HSU6102 Human DNA sequence ** 7.26e+ 7.26e+ 6.0 1442 95 HSU63108 Human eukaryotic init 1.61e+ 6.0 2019 84 STU51985 Solanum tuberosum Clo 1.61e+ 6.0 17084 60 DWMTGNME D.virginiana complete 1.61e+ 6.0 38851 92 HSL161C2 Human DNA sequence fr 1.61e+ 6.0 38851 92 HSL161C2 Caenorhabditis elegan 1.61e+		53	٠	7038	S	PFGP195A		. 26
6.3 15421 57 PFCOMPTRA P.falciparum complete 7.26e+ 6.3 22024 57 PFRVAR23A Plasmodium falciparum 7.26e+ 6.3 3739 34 HSU232G Human DNA sequence fr 7.26e+ 6.3 17253 8 HSAC23H Human DNA Sequence fr 7.26e+ 6.3 17253 8 HSAC23H Human DNA Sequence 7.726e+ 6.3 200434 45 HS415G Human DNA Sequence 7.726e+ 6.3 20139 45 HS415G Human DNA Sequence 7.726e+ 6.0 1147 39 B11004 Human DNA Sequence 7.726e+ 6.0 1147 39 B13042 T30M24-5p6.1 TAMU Ara 1.61e+ 6.0 147 39 B13042 T30M24-5p6.1 TAMU Ara 1.61e+ 6.0 1950 51 DDECMA D.discoideum ecmA pro 1.61e+ 6.0 17084 60 DWTGNME D.viriginiana complete 1.61e+ 6.0 28951 92 HSL161C2 Human DNA Sequence fr 1.61e+ 6.0 34860 50 CELR173 Caenorhabditis elegan 1.61e+		53	٠	8633	S	PFPFMDR1		.26e+
6.3 22243 57 PFAVAR23A Plasmodium falciparum 7.26e+ 6.3 28078 48 CEF21F12 Caenorhabolitis elegan 7.26e+ 6.3 37393 94 HSU232G Human DNA sequence fr 7.26e+ 6.3 172533 8 HSAC2381 Human DNA sequence ** 7.26e+ 6.3 201239 45 HS415G2 Human DNA sequence ** 7.26e+ 6.3 201239 45 HS415G2 Human DNA sequence ** 7.26e+ 6.0 1147 39 B11004 F19A23-T7 IGF Arabido 1.61e+ 6.0 1452 95 HSU63108 Human eukaryotic init 1.61e+ 6.0 1950 51 DDECMA D.discoideum ecmA pro 1.61e+ 6.0 2019 84 STU51985 Solanum tuberosum Clo 1.61e+ 6.0 28951 92 HSLI61C2 Human DNA sequence fr 1.61e+ 6.0 28951 92 HSLI61C2 Human DNA sequence fr 1.61e+ 6.0 28951 92 HSLI61C2 Caenorhabditis elegan 1.61e+		59	٠	15421	เว	PFCOMPIRA	complet	.26e+
6.3 28078 48 CEF21F12 Caenorhabditis elegan 7.26 6.3 37393 94 HSU232G2 Human DNA sequence fr 7.26 6.3 17253 8 HSAC2381 Human DNA sequence fr 7.26 6.3 202434 45 HS415G2 Human DNA sequence ** 7.26 6.3 201239 45 HS45D1 Human DNA sequence ** 7.26 6.0 512 39 B11004 F19A23-T7 IGF Arabido 1.61 6.0 1147 39 B13042 T30M24-Sp6.1 TAMU Ara 1.61 6.0 1452 95 HSU63108 Human eukaryotic init 1.61 6.0 2019 84 STU51985 Solanum tubercoum clo 1.61 6.0 28951 92 HSLIGNY Human DNA sequence fr 1.61 6.0 28951 92 HSLIGNY Human DNA sequence fr 1.61 6.0 28951 92 HSLIGNY Human DNA sequence fr 1.61 6.0 28951 92 HSLIGNY Human DNA sequence fr 1.61 6.0 28951 92 HSLIGNY Human DNA sequence fr 1.61 6.0 28951 92 HSLIGNY Human DNA sequence fr 1.61		53		22243	2	PFAVAR23A	Plasmodium falciparum	.26e+
6.3 3733 94 HSU233C2 Human DNA sequence fr 7.26 6.3 17253 8 HSAC2381 Human BAC clone RG020 7.26 6.3 200434 45 HS415G2 Human BAC clone RG020 7.26 6.3 200434 45 HS415G2 Human BAC sequence ** 7.26 6.0 512 39 B13004 Human DNA sequence ** 7.26 6.0 1147 39 B13004 T30M24-Sp6.1 TAMU Ara 1.61 6.0 1452 95 HSU63108 Human eukaryottc init 1.61 6.0 2019 84 STU51885 Solanum tuberosum clo 1.61 6.0 28951 92 HSL6102 Human DNA sequence [1.61 6.0 28951 92 HSL6102 Human DNA sequence [1.61 6.0 34860 50 CELR173 Caenorhabditis elegan 1.61		50	٠	28078	4	CEF21F12	eleg	
6.3 95936 44 HS127L4 Human DNA sequence ** 7.26 6.3 200434 45 HS4C2381 Human BAC clone RG020 7.26 6.3 201239 45 HS415G2 Human DNA sequence ** 7.26 6.0 512 39 B11004 F19A23-T7 IGF Arabido 1.61 6.0 1147 39 B11004 T19A23-T7 IGF Arabido 1.61 6.0 1147 39 B13042 T30M24-SpC1 TAMU Ara 1.61 6.0 1950 51 DDECMA D.discoideum ecmA pro 1.61 6.0 2019 84 STU51985 Solanum tubersoum clo 1.61 6.0 17084 60 DVMTGNME D.virginiana complete 1.61 6.0 28951 92 HSLIGLOZ Human DNA sequence fr 1.61 6.0 34860 50 CELR173 Cemorhabditis elegan 1.61		53	٠	37393	6	HSU232G2	DNA sequence	.26e+0
6.3 172533 8 HSAC2181 Human BAC clone RG020 7.26 6.3 200434 45 HS415G2 Human DNA sequence ** 7.26 6.3 201239 45 HS435D1 Human DNA sequence ** 7.26 6.0 512 39 B11004 F19A23-T7 IGF Arabido 1.61 6.0 147 39 B13042 T30M24-Sp6.1 TAMU Ara 1.61 6.0 1452 95 HSU65108 Human eukaryotic init 1.61 6.0 2019 84 STU51985 Solanum tubercoum clo 1.61 6.0 28951 92 HSL16102 Human DNA sequence fr 1.61 6.0 28951 92 HSL16122 Cenorhabditis elegan 1.61 6.0 34860 50 CELR173 Cenorhabditis elegan 1.61		53		95936	4	HS127L4	DNA sequence	.26e+0
6.3 200434 45 HS415G2 Human DNA sequence ** 7.26 6.3 201239 45 HS435D1 Human DNA sequence ** 7.26 6.0 512 39 B11004 F19A23-T7 IGF Arabido 1.61 6.0 1147 39 B13042 T30M24-Sp6.1 TAMU Ara 1.61 6.0 1950 51 DDECMA D.discoideum ecmA pro 1.61 6.0 2019 84 STU51985 Solanum tuberosum Clo 1.61 6.0 28951 92 HSL6102 Human DNA sequence f 1.61 6.0 34860 50 CELR173 Caenorhabditis elegan 1.61 6.0 34860 50 CELR173 Caenorhabditis elegan 1.61 6.0 2013 94 50 CELR173 CAENOR C		58		172533		æ	BAC clone RG02	.26e+0
6.3 201239 45 HS435D1 Human DNA sequence ** 7.26 6.0 512 39 B11004 F19A23-T7 IGF Arabido 1.61 6.0 1147 39 B13042 T30M24-Sp6.1 TAMU Ara 1.61 6.0 1452 95 HSU63108 Human eukaryottc init 1.61 6.0 1950 51 DDECMA D.discoideum ecmA pro 1.61 6.0 28951 92 HSLIGHOR PUNTGINIANA COMPILE 1.61 6.0 28951 92 HSLIGHOZ Human DNA sequence fr 1.61 6.0 34860 50 CELR173 Cemorhabditis elegan 1.61		53		200434	4	HS415G2	DNA sequence	. 26
6.0 512 39 B11004 F19A23-T7 IGF Arabido 1.61e+0 6.0 1452 95 B13042 T30MA4-Sp6.1 TAMU Ara 1.61e+0 6.0 1452 95 B13042 Human eukaryotic init 1.61e+0 6.0 1950 51 DDECMA D.0discoideum ecmh pro 161e+0 6.0 2019 84 STU51985 Solanum tuberosum clo 1.61e+0 6.0 17084 60 DWMTGNME D.virginiana complete 1.61e+0 6.0 28991 92 HSLIGIS Caenorhabditis elegan 1.61e+0 6.0 34660 50 CELR173 Caenorhabditis elegan 1.61e+0		5		201239	4	HS435D1	DNA sequence *	26
6.0 1147 39 B13042 T30M24-Sp6.1 TAMU Ara 1.61e+0 6.0 1452 95 HSU63108 Human eukaryotic init 1.61e+0 6.0 1950 51 DDECMA D.discoideum ecmA pro 1.61e+0 6.0 2019 84 STDS1985 Solanum tuberosum clo 1.61e+0 6.0 17084 60 DYWTGNWB D.virginiana complete 1.61e+0 6.0 28951 92 HSL161C2 Human DNA sequence fr 1.61e+0 6.0 34860 50 CELRA73 Caenorhabditis elegan 1.61e+0		78	٠.	512	m	B11004	-T7 IGF	.61e+0
6.0 1452 95 HSU63108 Human eukaryotic init 1.61e+0 6.0 1950 51 DDECNA D.discoideum ecmA pro 1.61e+0 6.0 219 84 STU51985 Solanum tuberosum clo 1.61e+0 6.0 17084 60 DVWHCHME D.virginiana complete 1.61e+0 6.0 28951 92 HSLIGICZ Human DNA sequence fr 1.61e+0 6.0 34560 50 CELR773 Caenorhabditis elegan 1.61e+0		28		1147	m	B13042	-Sp6 1 TAMIT	610
6.0 1950 51 DDECMA D.discoideum ecmA pro 1.61e+0 6.0 2019 84 STU51985 Solanum tuberosum clo 1.61e+0 6.0 17084 60 DVMTGNME D.virginiana complete 1.61e+0 6.0 28951 92 HSLI61C2 6.0 34860 50 CELRA73 Caenorhabditis elegan 1.61e+0		28		1452	σ		eukarvotici	616
6.0 2019 84 STU51985 Solanum tuberosum clo 1.61c+0 6.0 17084 60 DVMTGNME D.virginiana complete 1.61c+0 6.0 28951 92 HSL161C2 Human DNA sequence fr 1.61c+0 6.0 34860 50 CELR173 Caenorhabditis elegan 1.61c+0		28		1950	2		PCMA	610+
6.0 17084 60 DVMTCNME D.virginiana complete 1.61e+0 6.0 28951 92 HSL161C2 Human DNA sequence fr 1.61e+0 6.0 34860 50 CELR173 Caenorhabditis elegan 1.61e+0		28	٠.	2019	œ	œ	mar so	619
6.0 28951 92 HSL161C2 Human DNA sequence fr 1.61e+0 6.0 34860 50 CELRR73 Caenorhabditis elegan 1.61e+0		28	Ξ.	17084	9	DVMTGNME	virginiana compl	4019
6.0 34860 50 CELR173 Caenorhanditis elegan 1.61e+0		8	•	28951	σ	HST.16102	man DNA segment	1010
Caenoria Caenoria Libration 1:01e+0		a		10000	ľ	5110	babat 10 0100) (
		9 0		0 10 10 10 10 10 10 10 10 10 10 10 10 10	γ,	1000	s ereda	T.ore

ALIGNMENTS

13-SEP-1996 (Rel. 49, Created)
10-JUL-1997 (Rel. 52, Last updated, Version 2)
Lycopersicon esculentum copia-like retrotransposon ToRTL1,
3-hydroxy-3-methylglutaryl CoA reductase 2 (HMG2) gene, complete Lycopersicon esculentum (tomato)
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; vascular plants;
seed plants; Magnoliophyta; Magnoliopsida; Solananae; Solanales;
Solanaceae; Solanum clade; Lycopersicon. BP. standard; DNA; PLN; 16720 LEU68072 U68072; g2246449 cds. RESULT ID DATE OF THE SERVICE OF THE SERVIC ä;

```
NVFNQSSRFARLQRIQCAIAGKNLYMRFVCSTGDAMGMNMVSKGVQNVLDYLQNEYPD
                                                                                                                                                                     DVIGISGNFCSDKKPAAVNWIEGRGKSVVCEAIITEEVVKKVLKTEVAALVELNMLKN
                                                                       QRITGKSLEGLPLEGFNYESILGQCCEMPIGYVQIPVGIAGPLLLNGKEFSVPMATTE
                                                                                                      CLVASTNRGCKAIYASGGATCILLRDGMTRAPCVRFGTAKRAAELKFFVEDPIKFETL
                                                                                                                                                                                                     TGSAMAGALGGFNAHASNIVSAVFIATGQDPAQNIESSHCITMMEAVNDGKDLHISVT
                                                                                                                                                                                                                                    PSIEVGTVGGGTQLASQSACLNLLGVKGANREAPGSNARLLATVVAGSVLAGELSLMS
        LLGFFGIGFVQTFVSRGNNDSWDENDEEFLLKEDSRCGPATTLGCAVPAPPARQIAPM
                                       PPQPSMSMVEKPAPLITSASSEEDEELIKSVVQGKIPSYSLESKLGDCKRAASIRKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEUG8072 16720 bp DNA PLN 09-JUL-1997
Lycopersicon esculentum copia-like retrotransposon TORTL1,
3-hydroxy-3-methylglutaryl COA reductase 2 (HMG2) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tettettttaacaattataettgteaateateaateceacaaacaacactttttetetee 12733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12434 caaatgcaaaatgtatgagttatttcataatagcccgagttcgtatccaaatattttaca 12493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tatattattgtaaaagataatactccattcaaaatataaaatgaaaaagtccagcgcgg 12613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 CAAATGCAAAATGTATGAGTTATTCATAATAGCCC-AGTTCGTATCCAAATATTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 TATATTATTGTAAAAGATAATACTCCATTCAAAATATAAAATGAAAAAGTCCAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 16720;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 428; DB 16; I
Pred. No. 1.91e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tettttteeteacegeegeagaettaeeggtgaaa 12769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 ICTITITCCICACCGGCGGCAGACTIACCGGIGAAA
                                                                                                                                                                                                                                                                    ISSGQLVNSHMKYNRSTKDVTKASS
                                                                                                                                                                                                                                                                                   13888..14069
/gene="HMG2"
                                                                                                                                                                                                                                                                                                                                 14272..14618
/gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 92.4%;
1 Similarity 99.1%;
452; Conservative
                                                                                                                                                                                                                                                                                                                    /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U68072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                FT
                                                                                                                                                                                                                               FT
FT
                                                                                                                                                                                                                    Σ
                                                                                                   뭅
                                                                                                                                    FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDVRRRSEEPVYPSKVFAADEKPLKPHKKQQQQEDKNTLLIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(12664..13805,13888..14069,14272..14618,15034..>15576)
/gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DALPLPLYLTNGLFFTMFFSVMYFLLSRWREKIRNSTPLHVVTLSELGAIVSLIASVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="3-hydroxy-3-methylglutaryl CoA reductase 2"
join(12772..13805,13888..14069,14272..14618,15034..15276)
/gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="3-hydroxy-3-methylglutaryl CoA reductase 2"
/db_xref="PID:e328266"
                                                                                                                                                                                                                                                               Submitted (19-JUN-1997) to the EMBL/GenBank/DDBJ databases.
Department of Biological Sciences, University of Illinois at
Chicago, 900 S. Ashland Ave, Chicago, IL 60607, USA Sequence update
by submitter
                        Ø
Daraselia N.D., Tarchevskaya S., Narita J.O.;
"The promoter for tomato 3 hydroxy-3-methylglutaryl coenzyme
reductase gene 2 has unusual regulatory elements that direct
high-level expression";
                                                                                                                                                Submitted (27-AUG-1996) to the EWBL/GenBank/DDBJ databases. Department of Biological Sciences, University of Illinois at Chicago, 900 S. Ashland Ave, Chicago, IL 60607, USA
                                                                                                                                                                                                                                                                                                                                                                                                                              site duplication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(11221..11226)
/note="putative insertion site duplication"
12627..12641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
/note="copia-like retrotransposon ToRTL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="PID:e328270"
complement(10397..10408)
note="putative primer binding site"
                                                                                                                                                                                                                                                                                                                                                                            /organism="Lycopersicon esculentum"
/strain="VFNT Cherry"
                                                                                                                                                                                                                                                                                                                                                                                              /strain="VFNT Cherry"
complement(1526..1531)
/note="putative insertion
complement(1532..2341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2342..2355)
/note="polypurine tract"
complement(2769..4592)
/note="ORF 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /pseudo
/db_xref="PID:e328269"
complement(7542..10349)
/note="ORF 1; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1532..11220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5092..7545)
/note="ORF 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="PID:e328599"
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                  Plant Physiol, 112:727-733(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="3' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="5" LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12664..13805
/gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0412..1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                1-16720
Narita J.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                     Narita J.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATA_signal
5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer_bind
                                                                                                     1-16720
                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
```

US-08-713-928A-5.rge

```
Direct Submission
Submitted (19-JUN-1997) Department of Biological Sciences,
University of Illinois at Chicago, 900 S. Ashland Ave, Chicago, IL
60607, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oin(12664..13805,13888..14069,14272..14618,15034..>15576)
                                                                                                                                                                                                                                                                                                                                                                                       님
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="3-hydroxy-3-methylglutaryl COA reductase 2"
join(12772..13805,13888..14069,14272..14618,15034..15276)
/gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                             Submitted (27-AUG-1996) Department of Biological Sciences, University of Illinois at Chicago, 900 S. Ashland Ave, Chicago,
                                                                               charophyta/Embryophyta group. Embryophyta; vascular plants; splants; Magnoliophyta; Magnoliopsida; Solananae; Solanales; Solanaceae; Solananae; Solananaeae; Solananaeae; Solananaeae; Solananaeae; Solananae; Solananae; Solanales; Solanaceae; Solananae; Johanaeae; Solanales; Johanaeae; Solanales; Solanaceae; Solanales; Daraeelia, N.D., Tarchevskaya,S. and Narita,J.O.
The promoter for tomato 3-hydroxy-3-methylglutaryl coenzyme A reductase gene 2 has unusual regulatory elements that direct high-level expression
Plant Physiol. 112 (2), 727-733 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1526..1531)
/note="putative insertion site duplication"
complement(1532..2341)
/note="3' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(11221..11226)
/note="putative insertion site duplication"
12627..12641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1532..11220)
/organism="Lycopersicon esculentum"
/note="copia-like retrotransposon ToRTL1"
complement(2342..2355)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(10397...10408)
/note="putative primer binding site"
10412..11220
/note="5' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Lycopersicon esculentum"
/strain="VFNT Cherry"
                                                              Eukaryotae; mitochondrial eukaryotes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="polypurine tract"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /pseudo
complement(7542..10349)
/note="ORF 1; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2769..4592)
/note="ORF 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /pseudo
complement(5092..7545)
/note="ORF 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence update by submitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                               Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 16720)
                                                                                                                                                                                                                                                                                                (bases 1 to 16720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'dene="HMG2"
                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..16720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2664..1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                             Narita, J.O.
                                                                                                                                                                                                                                                                                                                    Narita, J.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                           ORGANISM
                                                                                                                                                                                                                                                                    MEDITIVE
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                     'AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                           FERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REMARK
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                     .
```

```
/product="3-hydroxy-3-methylglutaryl CoA reductase 2"
/db xref="Ploig2246450"
/translation="MDVRRRSEEPVPSKVFAADEKPLKPHKKOQQQEDKNTLLIDA
/translation="MDVRRRSEEPVPSKVFAADEKPLKPHKKOQQQQEDKNTLLIDA
SDALPLPLYLTNGLFFYMFEVLSRWERLIKRSTPLHVTLSELGAIVSLIASV
IYLLGFFGIGFVQTFVSRGNNDSWDENDEFLLKSDVGCRTBYSTESKLGDCKRASIR
PMAPPOPSMGWNFSRAPLITSSASEBDEITISSVVGGTRESYSLESKLGDCKRASIR
KEVNGRITGKSLEGLPLEGRYESILGGCCEMPIGSVQIPOTAGGLAGGLAGGRINGKESVPM
ATTEGCLVASTNRGCKAIYASGGATCILLRDGWTRAPCVRFGTARRAELKFFVEDDI
KFETLANTFNQSRSFRALGRIQCAIAGKNIVARFVGSTGDAMGMNVSKGVONVLDYL
QNEYPDMDVJGISGNRCSDKRPAAVNWIEGRGKSVVCEAIITEGWNKVKLTFVAALV
ELNMLKNLTGSAMAGALGGFNAHASNIVSAYTIATGODPAQNIESSHCITMMEAVNDG
KDLHISYTWAPSIEVGTVGGGTQLASQSACLNLLGVKGANREAPGSNARLLATVVAGSV
LAGELSLMSALSSGQLVNSHMKYNRSTKDVTKASS"
13888. 14 0609
/gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   12613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caaccgggttcctctataaatacatttcctacatcttctcttctctccccacatccc 12673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOMHMG2A 2884 bp DNA PLN 14-OCT-1992 Tomato 3-hydroxy-3-methyl glutaryl coenzyme A reductase (hmg2) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tatattattgtaaaagataatactccattcaaaatataaaatgaaaaaagtccagcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACCGGGTTCCT - - ATAAATACATTTCCTACATCTTCTTCTTCTCCTCACATCCCATCAC
                                                                                                                                                                                                                                                                                                                                                                                            Length 16720;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-hydroxy-3-methylglutaryl coenzyme A reductase.
Lycopersicon esculentum (strain VFNT cherry) DNA.
Solanum lycopersicum
                                                                                                                                                                                                                                                                                                                                                                                            Score 428; DB 134;
Pred. No. 1.91e-194;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                   5401
                                                                                                                                                                                                                                                                                                                                                      р
                                                                                                                                                                                                                                                                                                                                                   2863
                                                                                                                                                                                                                                                             /number=3
15034..>15576
/gene="HMG2"
                                                                                                                                                                                                                                                                                                        /number=4
15277..>15576
/gene="HMG2"
                                                                                                                                                                                                                                    14272..14618
/gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                                                            92.4%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                   3310 c
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.4%;
Best Local Similarity 99.1%;
Matches 452; Conservative
                                                                                                                                                                                                                     /number=2
                                                                                                                                                                                                                                                                                                                                                   5146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g170451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M63642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                     3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417
                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12674
                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Пр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
```

~

```
184 bp DNA PLN 12-SEP-1996 esculentum 3-hydroxy-3-methylglutaryl CoA reductase partial cds and 5' untranslated region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-AUG-1996) Department of Biological Sciences, University of Illinois at Chicago, 900 S. Ashland Ave, Chicago,
                                                                                                                                                                                                                                                                                                                                                                                                        Eūkaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Solananae; Solanales; Solanaceae; Solanum clade;
                                                                                                285 AAAGICCAGCGCGCAACCGGGTICCI--ATAAATACATTICCTACATCTTCTCTCTCTCC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    To (bases 1 to 184)
Daraselia, N.D., Tarchevskaya, S. and Narita, J.O.
The Promoter for Tomato 3-Hydroxy-3-Methylglutaryl Coenzyme P. Reductase Gene 2 Has Unusual Regulatory Elements That Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="3-hydroxy-3-methylglutaryl CoA reductase 63..184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/product="3-hydroxy-3-methylglutaryl COA reductase
1 59 c 21 g 57 t
 TCAAAATATAAAATGAAAAAAGTCCAGCGGGGAACCGGGTTCCT--ATAAATACATTTC
                                  ctacatcttctctctcctcacatcccatcactcttttaacaattatacttgtcaat
                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 cactttttctctcctcttttcctcaccggcggcagacttaccggtgaaa 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Lycopersicon esculentum'
28..42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 156; DB 78; Le
Pred. No. 1.58e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High-Level Expression
Plant Physiol. 112 (1996) In
2 (bases 1 to 184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="HMGR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="HMG2"
173..>184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="HMG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.7%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63..184
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon.
                                                                                                                                                                                                                                                                                       Lycopersicon (HMG2) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Narita, J.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60607, USA
                                                                                                                                                                     cggtgaaa 308
                                                                                                                                                                                                      CGGTGAAA 452
                                                                                                                                                                                                                                                                        LEU68072
                                                                                                                                                                                                                                                                                                                                        g1532207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47
                                                                                                                                                                                                                                                                                                                                                                          tomato
                                                                                                                                                                                                                                                                                                                        U68072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
                                  181
                                                                   325
                                                                                                                                                                     301
                                                                                                                                                                                                    445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
REFERENCE
 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403
                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                       RESULT
                                                                                             g
                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                g
                                                                                                                                                                                                    ò
                                                                   à
                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"PID:g170452"
/translation-"MDYRRSEEDVYESKVFAADEKPLKPHKKQQQQGEDKNTLLIDA
SDALEDLYLTINGETTMFFSWYFELSRWRKIRNSTPLHVVTLSELGAIVSLIAS
VIYLLGFFGIGFVQTFVSRGNNDSWDENDEEFLLKEDSRCGPATTLGCAVPAPPARQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APMAPPQPSMSMVEKPAPLITSASSGEDEEIIKSVVQGKIPSYSLESKLGDCKRAASI
KEKPWQRIFGYGKSLEGLPLGFRYESILGQCCRAFIGYVQIPVOLAGPLLINGKEFSVP
RATTEGCLVASTURGGKALVSGGATCILLRGMTRAPCVRFGTARRAAELKFVEDP
IKFESLANVFNQSSRPARLQRTQCAIAGKNLYMLCCSTGDAMMNWVSKGVONVLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LONEYPDMDVIGISGNFCSDKRPAAVNWIEGRGKSVVCEAIITEEVVKKVLKTEVAAL
VELNMLKNITGSAMAGALGGRAHAASNIVSAVFIATGODPAQNIESSHCITMMEAVND
GKDLHISVTWPSITGYTVGGGTQLASQSACINLLGVKGANREAPGSNARLLATVVAGS
VLAGELSLMSAISSGQLVNSHMKYNRSTKDVTKASS"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="3-hydroxy-3-methylglutaryl coenzyme A reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcaaaatataaaatgaaaaagtccagcgcggcaaccgggttcctctataaatacatttc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 TAATAGCCCAGTICGTATCCAAATATTTTACACTTGACCAGTCAACTTGACTATATAAAA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                              Yang, 2., Park, H.S., Lacy, G.H. and Cramer, C.L.
Differential activation of potato 3-hydroxy-3-methyl glutaryl
coenzyme A reductase genes by wounding and pathogen challenge
Plant Cell 3, 397-409 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taatagcccagttcgtatccaaatattttacacttgaccagtcaacttgactatataaaa
                                                                                                                                                                                        encoding
               Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Solananae; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1347,1430..1611,1813..2159,2575..2817)
                                                                                                                                                                                                                                                                                                                                                                       join(311..1347,1430..1611,1813..2159,2575..2817)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2884;
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                             Park, H.S., Denbow, C.J. and Cramer, C.L. Structure and nucleotide sequence of tomato HMG2 3-hydroxy-3-methyl-glutaryl coenzyme A reductase Plant Mol. Biol. 20, 327-331 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 294; DB 84; Pred. No. 2.35e-126; O; Mismatches 0;
                                                                                                                                                                                                                                                                                    /organism="Solanum lycopersicum"
(strain="VFNT cherry"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 881
                                                                                                                                                                                                                                                                                                                                                                                                        /EC_number="1.1.1.34"
                                                                                                                                                                                                                                                   Location/Qualifiers
1..2884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614
                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="hmg2"
1348..1429
/gene="hmg2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1612..1812
/gene="hmg2"
/number=2
1813..2159
/gene="hmg2"
                                                                                                                                                                                                                                                                                                                                    /gene="hmg2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1430..1611
/gene="hmg2"
                                                                                                                                                                                                                                                                                                                                                                                      gene-"hmg2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2160..2574
/gene="hmg2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.5%;
larity 99.4%;
Conservative
                                                                                                                                                                                                                                                                                                                     201..1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=3
                                                                                                                                                                                                                                                                                                                                                         /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oin(31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 306; Conser
                                                  (sites
                                                                                                                                   93005707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                829
                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                 JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                 AUTHORS
TITLE
                                                                                                                                 MEDLINE
REFERENCE
                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                  REFERENCE
                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

II

5

Õ

⋖

ä

2

ö

,

US-08-713-928A-5.rge

```
A39.7.0

G10 gene; LSU rRNA gene; ORF105; ORF129; ORF78; ORF79; ORF91; rpl14

gene; rpl16 gene; rpl2 gene; rpl33 gene; rpl36 gene; rp4 gene;

rpf0 gene; rps11 gene; rps12 gene; rps17 gene; rps19 gene;

gene; rps4 gene; RPS5 gene; rps7 gene; rps8 gene; tRNA-Asp;

tRNA-Cys; tRNA-G1n; tRNA-G1u; tRNA-G1y; tRNA-His; tRNA-Leu;

tRNA-Lys; tRNA-Met; tRNA-Phe; tRNA-Pro; tRNA-Ser; tRNA-Thr;

tRNA-Trp; trnA-Tyr; tufa gene.
                                                                                                                                                                                                                                                                                      /codon_start=1
/ppoduct="cell adhesion molecule gp80"
/db_xref="cell" gp7290"
/db_xref="plb:gp7290"
/db_xref="swiss-prot:p08796"
/db_xref="swiss-prot:p08796"
/db_xref="swiss-prot:p08796"
/db_xref="swiss-prot:p08796"
/db_xref="swiss-prot:p08796"
/db_xref="swiss-prot:p08796"
/db_xref="swiss-prot:p08797977777
/dcastalton="wrethurdspossions and possions are possions and possions and possions and possions are possions and possions and possions are possions and possions and possions are possions are possions and possions are possions are possions and possions are possions and possions are 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASVTMGSHIYTGLTVQDDGTNCHVIFTTRSVYESSNTITAKASTGVDMIYLDNQGNQQ
PITFTYNPPTITSTKQVNDSVEISTTNTGTDFTQISLTMGTSSPTNLVITGTNEKIVI
TLPHALPEGEIQFNLKAGISNVVTSTLLVTPVINSYTQAPHNGGSITISGIFLNNAHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JAN-1996) R.J.M. Wilson, National Institute for Medical Research, Mill Hill, London NW7 1AA, UK Related sequences X90351-X90354 (incl.), and X87630-X87631 (incl.). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNTIAGGLLNLELIQPFGFSTIVTSKSVFSPTITSITPLAFDLTPTNVTVTGKYFVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIVVDQNITDIVCAPDSNGESIICPVEAGSGTINLVVTNYKNFASDPTIKTEATTSTT
YTIPDTPTPTDTATPSPTPTETATPSPTPKPTSTPEETEAPSSATTLISPLSLIVIFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete gene map of the plastid-like DNA of the malaria parasite plasmodium falciparum J. Mol. Biol. 261 (2), 155-172 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 ITITITCATITITATATITITGAAIGGAGTATIATCTITIACAATAATATATACTITITIT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malaria parasite.
Plasmodium falciparum
Eukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFCOMPIRB 14001 bp DNA INV 14-FEB-1
P.falciparum complete gene map of plastid-like DNA (IR-B).
X95276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemosporida; Plasmodium.

1 (bases 1 to 14001)

Wilson, R.J.M., Denny, P.W., Preiser, P.R., Rangachari, K., Roy, A., Whyte, A., Strath, M., Moore, D.J., Moore, P.W. and Williamson, D.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 51; Length 370
Pred. No. 2.02e-02;
0; Mismatches 29; Indels
organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1137 ttttttttttttaaattaaaattttataaattca 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g 1323 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397
                                            rara_signal 1161..1168
prim_transcript 1179..>2868
prim_transcript 1180..>2868
prim_transcript 1193..>2868
prim_transcript 1194..>2868
gene //gene="gp80"
CDS //gene="gp80"
                        /strain="AX-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 14001)
Wilson, R.J.M.
                                                                                                                                                                                                                                                              /gene="gp80"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.8%;
Best Local Similarity 69.1%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96346169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207,
                                                                                                                                                                                                                                                     1 (bases 1 to 1095)
Faix,J., Gerisch,G. and Noegel,A.A.
Overexpression of the CSA cell adhesion molecule under its own camp-regulated promoter impairs morphogenesis in dictyostellum J. Cell Sci. 102, 203-214 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            摄.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDICSA 1095 bp DNA PLN 16-JUL-1992 Dictyostelium discoideum cAMP-regulated promoter (csA) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1992) C. Siu Besst Inse, 112 College St. Rn Toronto, Ontario, Canada M5G 1L6, CANADA 2 (bases 1 to 3700)
Desbarats, L., Lam, T.Y., Wong, L.M. and Siu, C.H.
Identification of a unique cAMP-response element in the gene encoding the cell adhesion molecule gp80 in Dictyostelium
                                                                                                                                                  CAMP-regulated promoter; cell adhesion molecule.
Dictyostelium discoideum (strain AX2) early development DNA.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Dictyostellida;
                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Dictyostellida;
Dictyostellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Dictyostelium discoideum"/strain-"AX2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem. 267 (27), 19655-19664 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 76;
Pred. No. 2.02e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 895 ttttttttttttttaaattaaaattttataaattca 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="early development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gp80 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (02-JUN-1992) C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell adhesion molecule; g
Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="csa"
/codon_start=1
a 69 c 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3700 bp D.discoideum gp80 gene. x66483 S45379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="csa"
905..1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="csa"
884..890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.18;
Matches 69; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 3700)
Siu Besst Inse, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="csa"
1084..1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /partial
                                                                       partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol.
                                                                                                M87525
q167697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                           SQURCE
ORGANISM
                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANI SM
                                                                                                                                                                                                                                                                                    REFERENCE
_ AUTHORS
_ TITLE
                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
FATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

Roberts, K.,

US-08-713-928A-5.rge

18191888 /gene="tRNA-Glu" 18191888 /gene="tRNA-Glu" /product="transfer RNA-Glu" 19011972 /gene="tRNA-Pro" 19011972 /gene="tRNA-Pro" 19992571 /gene="rpun fer RNA-Pro" 19992571	/gene="rpl4" /codon_start-1 /db_xref="PID:e220176" /db_xref="PID:e2171593" /translation="MAIIILNWYLNIIFKYKYNFFIKLYFNNYIKICKLIIYIIKY LYTNIYMYKHTKNKSKYFSNKKIRVOKGLGKRALKNFSPVCKGGACNFGPFYKEN KYILININKLFNKHTKNKSNYIIIKKLENIINLANFYKNKNYCIFKLLYKGIINN KYILININKLFNKHTKNKSNYIIIKKLENIINLANFYKNKNYCIFKLLYKGIINN KYILININKKFNKHTKNKSNYIIIKKLENIINLANFYKNKNYCIFKLLYKGIINN KYILININNKFNKHTKINIINTNYLYININKNYLIFTI" /Gene="rpl3" /db_xref="pID:e220177" /db_xref="pID:e12171594" /db_xref="pID:e1171594" /db_x	27993536 /gene="rpl2" /codon_start=1 /db_xref="rpl2" /db_xref="rpl2" /db_xref="rpl2" /db_xref="rpl2" /db_xref="rpl2" /db_xref="rpl2" /db_xref="rpl2" /db_xref="rpl2" /db_xref="rpl2" /ranslation="rpl2" /ranslation="rpl2" /gene="rpl2" /codon_start=1 /db_xref="rpl2" /db_	35573829 /gene="rps19" 38394483 /gene="rps3" /gene="rps3" /gene="rps3" /gene="rps3" /gene="rps3" /db_xref="rp10:e220180" /	45104899 45104899 /gene="rpl16" /codon_start=1 /db_xref="PID:e220181" /db_xref="PID:g1171598" /db_xref="PID:g1171598" /db_xref="PID:g1171598" /translation="MYNITIKKNOKGKIKGKFNLKFLSLYWGIISLDSGFL/TKNOLET SKFIINKYLKKIGYYKICIRCIKSLTKKSLKTRMGSGKGSIELYVSPIKKNKLLFEIS KISNNITYTTKVLSYKLPFKLQYIRK" 45104899 /gene="rpl16" 49135137
gene trnA gene trnA cobs	gene	CDS CDS	gene gene CDS	CDS gene gene
114001 /organism="Plasmodium falciparum" /strain="C10"	242.314 /gene="trNA-Thr" 340966 /gene="tpS4" /codon_start=1 /db_xref="pib:e220175" /db_xref="pib:e220175" /db_xref="pib:e220175" /db_xref="pib:e220175" /db_xref="pib:e220175" /translation="MIKFINENRILILILILILILILILILILILILILILILILILILIL	/gene="tRNA-Cys" 1072.1142 /gene="tRNA-Cys" /product="transfer RNA-Cys" /product="transfer RNA-Cys" 1148136 /gene="tRNA-Leu" /note="extein 1" /product="transfer RNA-Leu" /gene="tRNA-Leu"	/gene="tRNA-Met (1)" 13731452 /gene="tRNA-Met (1)" /product="transfer RNA-Met (1)" 14571541 /gene="tRNA-Tyr" 14571541 /gene="tRNA-Tyr" /product="transfer RNA-Tyr" 15551646 /gene="tRNA-Ser" /product="transfer RNA-Ser" /product="transfer RNA-Ser" /product="transfer RNA-Ser"	/gene="txna-ser" 16531728 /gene="txna-asp" 16531728 /gene="txna-asp" /product="transfer RNA-asp" /gene="txna-tys" 17391811 /gene="txna-tys" /product="txna-tys"
	CDS CDS gene gene trana	gene trna trna trna trna	tRNA gene tRNA tRNA	gene tRNA gene tRNA

```
/db_xref-"Swiss-Prot:002465"
/db_xref-"Swiss-Prot:002465"
/tanslation="Wenningerpowssefpartotsssaaaxdnsshfekegslar
Wegdlklreralanngsaaditghtvypapatahproganfpssymikuleedial
Retrolykreifyfelmbaaalvynwvsigityysaydnrfelalexmivovptlyfel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKLYRAASVPERARKSYAYLMALLGVVLFNIIFFVGFKRSGMNGLIWVISLFHNDHNA
Development 120 (10), 2891-2900 (1994)
95331128
5 (bases 1091 to 2379)
Fichardson, D.L. and Loomis, W.F.
Disruption of the sporulation-specific gene spiA in Dictyostellum descoideum leads to spore instability
Genes Dev. 6 (6), 1058-1070 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="expressed immediately prior to spore formation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGAMATVSLFFWFVGVFLTIALFIMYLRLNNTKRQRGEIQNAGFREYIKSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-1997
F25H9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thale cress.
Arabidopsis thaliana
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS
genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 51; Length 237
Pred. No. 6.22e-01;
0; Mismatches 26; Indels
                                                                                                                                Location/Qualifiers
1..2379
/organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                u
                                                                                                                                                                                                                                                                                                                                                                                                                  join(1091..1632,1753..2353)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1632,1753..2210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B12074 1124 bp DNA
F25H9-T7.2 IGF Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="spiA protein"
/db_xref="PID:97164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 CTCCATTCAAAATATAAATGAAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247
                                                                                                                                                                                              /clone="pLGL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                             /gene="Dd31"
/gene="Dd31"
1091..167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     662 ttaaattaaaaaaaaaaaaaa
                                                                                                                                                                                /strain="Ax4"
                                                                                                                                                                                                                                                                                  /gene="Dd31"
1057..1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=2
2348..2353
/gene="spiA"
a 266 c
                                                                                                                                                                                                                                                        /gene="Dd31"
790..1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number=1
1753..2353
/gene="spiA"
                                                                                                                                                                                                                           /gene="Dd31"
                                                                                                                                                                                                                                                                                                                                                     /gene="spiA"
                                                                                                                                                                                                                                                                                                                                                                                                  /gene="spiA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="spiA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="spiA"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="spiA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9%;
ilarity 69.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                       /numper=
                                                                                                                                                                                                              ..1263
                                                                                                                                                                                                                                             .1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g2093194
GSS.
                                                                                                                                                                                                                                             prim_transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B12074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                        TATA_signal
                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                    AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                        REFERENCE
                                                                                                                 MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                        MEDLINE
                                                                                                   JOURNAL
         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                              /db_xref="PID:g1171599"
/translation="MNIKIGYVIKNLNINIKIVCISFYKYNFKYKKLLLCNLYIKIYD
NRNEIIINDYILFKYYKKSKYCNNKVIKIL"
                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:91171601"
/translation="MIKFENNVKYNFKLKKNFILYKYNKVIYYLSILLYNYKYIFKL
                                                                                                                                                           /codon_start=1
/db_xref="PiD::220183"
/db_xref="PiD::2171600"
/translation="MIYINSILDVIDNSGIFKFKYICTLNKYKNPKYGDIVIGVVYSL
                                                                                                                                                                                                                        YNNNLYKKSDKCKGILVQQKKFLNFKKYYSIKFNKNAVIIINNKLNFVGTKSNNYISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prespore; spiA gene; sporulation-specific prespore gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-AUG-1990) Richardson D.L., University of California,
San Diego, Dept. of Biology 0322, 9500 Gilman Drive, La Jolla, CA
92093-0233, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 / Ri
2715,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B1-10, National Institutes of Health, 6 Center Drive MCS 27/
Bethesda, MD 20892-2715, USA
4 (Dases 1091 to 2379)
Richardson, D.L., Loomis, W.F. and Kimmel, A.R.
Progression of an inductive signal activates sporulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bld
MCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ō
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 14001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sukaryotae; mitochondrial eukaryotes; Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCDB/NIDDK,
enter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richardson, D.L., Hong, C.B. and Loomis, W.F.
A prespore gene, Dd31, expressed during culmination
Dictyostellum discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D31 2379 bp DNA IN
discoideum culmination spiA (Dd31) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 57;
Pred. No. 2.68e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-FEB-1996) Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Biol. 144 (2), 269-280 (1991)
                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:e220199"
                                                                   db_xref-"PID:e220182'
                                                                                                                                                                                                                                                                                                                                                                                                 annotations omitted,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Revised by [3]
2 (bases 1091 to 2379)
                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                      /codon_start=1
                                                                                                                                              /gene="rpl14"
                                                                                                                                                                                                                                                                     /gene="rpl14"
                                   /gene="rps17"
                                                                                                                                                                                                                                        YIKYKLNMNKFK"
5134..5478
                                                                                                                                                                                                                                                                                   5492..5878
/gene="rps8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 2379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2379)
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%;
Best Local Similarity 67.7%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richardson, D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richardson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dd31 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g1177288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91184533
                                                                                                                                                                                                                                                                                                                                                                                         Note: remainder of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                     CDS
                    CDS
                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
```

ద ö 8 ò

```
/product-"cytosolic glycoprotein FP21"

/db_xref-"PiD:g1658022"

/db_xref-"PiD:g1658022"

/dranslation-"MSLVKIESSDERVFEIEKEIACMSVTIKNMIEDIGESDSPIPLP

/VTANSLAILEKYLDVCHHHQIPSPQGDDKKDEKRLDDIPPYDRDFCKYDQPILFELILA
ANYLDIKPLLDVTCKTVANMIRGKTPEEIRKIFNIKNDFTPEEEEQIRKENEWCEDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="Maprksnvylslynsytidspopssinywwkmgsllglluviol
VTGIFMAMHYSSNIELAFSSVBHIMRDVHSGYILRYLHANGASFFFWVMFMHMAKGLY
VTGIFMAMHYSSNIELAFSSVBHIMRDVHSGYILRYLHANGASFFFWVMFMHMAKGLY
VGSYRSPRVTIMNVGYIFILIIATAFLGYCOVYGOMSHWAGATVITHDFSAIPPVGND
IVSWLWGGSVSNPTIORFFALHYLDYPIIAAMYIMHLMALHIGSSNPLGITGNLDR
IPPMHSYFIKDLYFFFFFLIATAFVTPYSPWYLL
PFYAILRSIPDKLLGVITMFAAILVLVLPFTDRSVVRGNIFKVLSKFFFFFFFFFFFFFF
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..6615
/organism="Saccharomyces douglasi1"
/mitochondrion
join(1..393,1705..1726,2507..2520,3973..4049,5662..6313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-APR-1991) J. Lazowska, CNRS Centre de Genetique, Moleculaire, 91198 Gif Sur Yvette, FRANCE
2 (bases) Lo 6615)
Tian, G.L., Michel, F., Macadre, C., Slonimski, P.P. and Lazowska, J. Incipient mitochondrial evolution in yeasts. II. The complete sequence of the gene coding for cytochrome b in Saccharomyces douglasii reveals the presence of both new and conserved introns and discloses major differences in the fixation of mutations in
                                                                                  /gene="fpa1"
/note="SKP1-like; glycosylated; mRNA sequence deposited
under GenBank Accession Number U18063"
                                                                                                                                                                                                                                                                                                                                                                                                                                         LLGQIGACHVEVPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIGRVNK"
<1..393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytochrome b.
Saccharomyces douglasii.
Mitochondrion Saccharomyces douglasii
Bukaryotae; mitochondrial eukaryotes; Fungi; Ascomycota;
Hemiascomycetes; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 51; Length 1891; Pred. No. 1.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. 218 (4), 747-760 (1991)
                                                                                                                                                                                                                                                                                             760 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon=(seq:"tga",aa:Trp)
/product="cytochrome b"
/db_xref="PID:g13618"
/transl_table=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISDCYTB 6615 bp DNA
S.douglasii gene for cytochrome
X59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                           191 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       956 ttaaaatttttttttttaaattttt 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                 /codon_start=1
                                            /gene="fpa1"
1160..1648
                                                                                                                                                                                                                                                                                                                                                        6.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces.
1 (bases 1 to 6615)
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 68.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                           251 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lazowska, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Mol. Bi
91218158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       evolution
                                                                                                                                                                                                                                                                                             689
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1891)
West, M.C., Kozarov, E. and Teng-umnuay, P.
The cytosolic glycoprotein FP21 of Dictyostelium discoideum is encoded by two genes resulting in a polymorphism at a single amino
                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum cytosolic glycoprotein FP21 (fpa1) gene,
Charophyta/Embryophyta group; Embryophyta; vascular plants; seed
plants; Magnoliophyta; Magnoliopsida; Capparales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Columbia"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
/clone="F25H9"
                                                                                  Sun, H.
                                                                                                                                                                                                                                                                          PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 TITITICATITIATATITIGAATGGAGTATTATCTITIACAATAATATACTTICTTTTT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-007-1996) Anatomy & Cell Biology, University of Florida, 1600 SW Archer Rd., Gainesville, FL 32610-0235, USA Location/Qualifiers
                                                                                                                                                                                                                                        University of Pennsylvania Dept. of Biology, University of Pennsylvania, Philadelphia, 19104
                                                                                                                                                                Other_GSSs: F25H9-T7, F25H9-T7.1, F25H9-Sp6, F25H9-Sp6.1,
                                                                                  L1, Y., Shinn, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Dictyosteliida;
Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Dictyostelium discoideum"
/strain="Ax3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 39;
Pred. No. 1.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid position
Unpublished (1996)
2 (bases 1 to 1891)
West, M.C., Kozarov, E. and Teng-umnuay, P.
Direct Submission
                                                         [ (bases 1 to 1124)
Feng,J., Dewar,K., Buehler,E., Kim,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 t
                                                                                                                                                                                                                                                                                                      Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
                                                                                                                                                                                                      Contact: Ecker J.
Arabidopsis Thallana Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 78
High quality sequence stop: 371.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="IGF"
/sex="hermaphrodite"
www.264 c 61 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       599 ttttnntttttnnntttnnttntt 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 ITITAATITITGAAGTAAAGTTTT 203
                                                                                                                        BAC End Sequences at ATGC Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoldeum. Dictyostelium discoldeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1891 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 6.7%;
Best Local Similarity 56.5%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..1891
                                                                                                                                                                                                                                                                                                                                                                       Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete cds
                                            Arabidopsis.
                                                                                                                                                                                     F25H9-Sp6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91658021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDU73685
                                                                                                       Ecker, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID
KEYWORDS
SOURCE
- ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                           REFERENCE
                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
```

윱 g 셤 გ ö

US-08-713-928A-5.rge

```
CEF02H6 50751 bp DNA HTG 27-NOV-1996
*** SEQUENCING IN PROGRESS *** Caenorhabditis elegans cosmid F02H6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ge-Unfinished; Author=Cummings PN; LastModification=Nov 22 12:08
Cosmid=F02H6; Contig ID=00092; Length=3538; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ge-Unfinished; Author=Cummings PN; LastModification=Nov 22 12:08
Cosmid=F02H6; Contig ID=00078; Length=1924; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status=Cambridg
e-Unfinished; Author=Cummings PN; LastModification=Nov 22 12:08
cOsmid=F02H6; Contig ID=00319; Length=1898; Order=Unknown; •
Status=Cambrids
Cosmid=F02H6; Author=Cummings PN; LastModification=Nov 22 12:08
Cosmid=F02H6; Contig ID=00340; Length=1677; Order=Unknown;
Status=Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status=Cambridg
e-Unfinished; Author=Cummings PN; LastModification=Nov 22 12:08
Cosmid=F02H6; Contig ID=00456; Length=17726; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status=Cambridg
Status=Cambridg
e-Unfinished; Author=Cummings PN; LastModification=Nov 22 12:08
cosmid=F02H6; Contig ID=00247; Length=10792; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 12:08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e-Unfinished; Author-Cummings PN; LastModification=Nov 22 12:08
Cosmid=F02H6; Contig ID-00454; Length=1393; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e-Unfinished; Author=Cummings PN; LastModification=Nov 22 12:08
Cosmid=F02H6; Contig ID=01032; Length=4639; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * This sequence is unfinished. When sequencing is complete,
* the sequence data presented in this record will be replaced
*by a single finished sequence with the same accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sanger
                                                                                Db 25173 tacataaacataatataaattataatataaattataaagtacagttcaaatt 25227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-NOV-1996) Nematode Sequencing Project, Sanger Hinxton, Cambridge CB10 1RQ, England and Department of Genwashington University, St. Louis, MO 63110, USA. E-mail: Besseanger.ac.uk or rwwenmatode.wusl.edu order of segments is not known; 800 n's separate segments. Cosmid=F02H6; Contig ID=00011; Length=1507; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *** WARNING: Phase 1 High Throughput Genome Sequence ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status=Cambridg
e-Unfinished; Author=Cummings PN; LastModification=Nov
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                          Length 50751;
  Length 36238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6586 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 42; Length 507
Pred. No. 1.43e+00;
0; Mismatches 12; Indels
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans"
                                           0; Mismatches 12;
                     Pred. No. 1.43e+00;
    DB 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g 13831 t
Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="IV"
8507 c 8392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="F02H6"
                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 50751)
  Query Match 6.7%;
Best Local Similarity 78.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.7%;
Best Local Similarity 78.2%;
Matches 43; Conservative
                                             43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status-Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status=Cambrid
                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis.
                                                                                                                                                                                                                                                   HTGS phase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ø
                                                                                                                                                                                                                                                                                              g1695011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13435
                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                             å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-NOV-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dge-Unfinished; Author-Basham VM; LastModification=Nov 13 14:59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ge-Unfinished; Author=Basham VM; LastModification=Nov 13 14:59
Cosmid=K01G12; Contig ID=00966; Length=34991; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is unfinished. When sequencing is complete, the sequence data presented in this record will be replaced by a single finished sequence with the same accession number.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEKOIG12 36238 bp DNA HTG 27-NOV-1996
*** SEQUENCING IN PROGRESS *** Caenorhabditis elegans cosmid
KOIG12; HTGS phase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Order of segments is not known; 800 n's separate segments. Cosmid=K01G12; Contig ID=00976; Length=1039; Order=Unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAATACGATATTACCGAATATTATACTAAATCAAAATTTAATTTATCATATCAAT-TATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *** WARNING: Phase 1 High Throughput Genome Sequence ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6615;
                                                                                                                                                                                                                                                                                                                                                                                                             804 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       767ganism="Caenorhabditis elegans"
/clone="K01G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6492 g 10558 t
                                                                                                                                                                                                                                                                                                                                                           2664 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             ρ
                                                                                                                                                                                                                                                                                                                                                           616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                            /number=4
5662..>6313
/number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 36238)
                                                                                                                                                                                                                           3973..4049
/number=4
4050..5661
                                                        1705..1726
/number=2
                                                                                                                                          2507..2520
/number=3
2521..3972
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.7%;
Best Local Similarity 66.4%;
Matches 73; Conservative
                                                                                                 1727..2506
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6852 c
                                                                                                                                                                                                                                                                                                                                                           508 c
                                    'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status=Cambrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status-Cambri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11532 a
                                                                                                                                                                                                                                                                                                                                                             ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91695062
                                                                                                                                                                                                                                                                                                                                                           2827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                        intron
                                                                                                      intron
                                                                                                                                                                                    intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                   Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
TOURNAL
                                                            exon
                                                                                                                                               exon
                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                 DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠,
```

g ò

ò

```
219 AAATTAAAAAAAAAAAGTATATTATTGTAAAAGATAATACTCCATTCAAAATATAAA 278
                                                                                                                                                                                                                                                                                                                     standard; DNA; PLN; 192
                                                                                                                              279 ATGAAAAA 287
                                                                             879 ataaataaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          high-level
                                                                                                                                                                                                                                                                                 T 15
LEU68071
                                                                                                                                                                                                                                                                                                                                                                                               91532206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                        RESULT 110 DE 11
                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * This sequence is unfinished. It consists of 9 contigs for which the order is not known; their order in this record is arbitrary. In some cases, the exact lengths of the gaps * between the contigs are also unknown; these gaps are presented * as runs of N as a convenience only. When sequencing is complete, the sequence data presented in this record will be replaced *by a single finished sequence with the same accession number.

2067 (4836: contig of 2066 bp in length 6833 9032: contig of 2180 bp in length 6833 9032: contig of 14024 bp in length 18492: contig of 14024 bp in length 54339: contig of 21824 bp in length 54340 77292: contig of 22833 bp in length 17292: contig of 22833 bp in length 17292: contig of 22833 bp in length 17292: contig of 33770 bp in length 17292: contig of 33770 bp in length 17292: contig of 33770 bp in length 17293: contig of 20204 bp in length 17293: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans, G.A., Bradbury, P., Brignac, S., Bumeister, R., Burbee, D., Davlee, J., Davles, J., Davlas, C., Fondon, T., Franklin, T.L., Garner, H.R., Gordon, M., Gotway, G., Grant, O., Hahner, L., Harris, J., Hinson, S., Megarity, C., Narayanawamy, U., Mewton, J., O'Brien, K., Oliver, T., Patel, P., Probst, S., Rayner, S., Schageman, J., Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T. and Wilson, R.
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans, G.A., Bradbury, P., Brignac, S., Bumeister, R., Burbee, D., Davies, J., Davies, C.J., Davis, C., English, C., Fondon, T., Franklin, T.L., Garner, H.R., Gordon, M., Gotway, G., Grant, O., Hahner, L., Haris, J., Hinson, S., Megarity, C., Marayanaswamy, U., Newton, J., O'Brien, R., Oliver, T., Patel, P., Probst, S., Rayner, S. Schageman, J., Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-APR-1997) Genome Science and Technology Center, University of Texas Southwestern Medical Center at Dallas, 5323 Harry Hines Blvd, Dallas, TX 75235-8591, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29309 aaatttgaactgtcatttttataatttatattataatttatatttatgtttatgta
                                                                     *** WARNING: Phase 1 High Throughput Genome Sequence ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 111062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25179 c 26243 g 28168 t
                                                                                                                                                                                                                            HSACO01237 111062 bp DNA
*** SEQUENCING IN PROGRESS *** Hu
HTGS phase 1, 9 unordered pieces.
AC001237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/clone="pDJ891a18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 111062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 111062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 72.5%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31441 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Template
                                                                                                                                                                                                                                                                                                                                                                                                                               91945035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  요
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product_"3-hydroxy-3-methylglutaryl-CoA reductase 1" 181..>192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="3-hydroxy-3-methylglutaryl-CoA reductase 1"
/db_xref="PID:e265716"
/translation="MDVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
   13-SEP-1996 (Rel. 49, Created)
LyOUL-1997 (Rel. 52, Last updated, Version 4)
LyCopersicon esculentum 3-hydroxy-3-methylglutaryl-CoA reductase 1
(HMG1) gene, partial cds and 5' untranslated region.
                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; vascular plants;
seed plants; Magnoliophyta; Magnoliophyta; Magnoliopsida; Solananae; Solanales;
Solanaceae; Solanum clade; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                        Daraselia N.D., Tarchevskaya S., Narita J.O.;
"The promoter for tomato 3-hydroxy-3-methylglutaryl coenzyme
reductase gene 2 has unusual regulatory elements that direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-AUG-1996) to the EMBL/GenBank/DDBJ databases. Department of Biological Sciences, University of Illinois at Chicago, 900 S. Ashland Ave, Chicago, IL 60607, USA Chicago, Rey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 16; Lengum ...

Dred. No. 3.24e+00;

Lake 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 CIATAAATACATTTCCTACATCTTCTCTTCTCCTCACATCCCATCACT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 ctataaatacatttcttctactttcgcttctccacacaaaccatcact 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..192
/organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 192 BP; 46 A; 54 C; 20 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: Tue Feb 3 19:44:28 1998
                                                                                                                                                     Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   high-level expression";
Plant Physiol. 112:727-733(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HMG1"
/note="HMGR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="HMG1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.5%;
Best Local Similarity 81.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
[3-SEP-1996 (Rel. 49, 10-JUL-1997 (Rel. 52,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Job time : 1370 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Narita J.O.;
```

U	υυ
我们我们我们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人们	(ME)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Tue Feb 3 19:44:49 1998; MasPar time 66.98 Seconds 797.669 Million cell updates/sec abular output not generated.

>US-08-713-928A-5 (1-463) from US08713928A.seq 463 Description: Perfect Score: N.A. Sequence:

1 CAATACGATATTACCGAATA........CGGGGGAAAGTAAGGACGTC 463 GTTATGCTATAATGGCTTAT.......GGCCACTTTCATTCGTCWAG

TABLE default Gap 6 Scoring table:

159651 seqs, 57698962 bases x 2 Dbase 0; Query 0 STD : Searched: Nmatch

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseg30 1:part1.2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33

Mean 8.315; Variance 7.573; scale 1.098

atistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES			
			ф						
Res	Result		Query						
1	Ş.	Score	Match	Match Length DB	DB	e e	Description	Pred. No.	
		463	100.0	463	32	T71752	MegA promoter.	1.04e-198	
	~	434	93.7	1388	13	081473	HMG2 promoter I.	4.13e-185	
ძ	m	45	9.7	1047	~	010572	Human Natriuretic Pep	1.47e-07	
	4	42	9.1	1047	~	010572	Human Natriuretic Pep	2.29e-06	
	'n	41	8.9	204		N81164	Base substituted E.co	5.66e-06	
	o	35	7.6	91	σ	051746	Oligonucleotide probe	1.18e-03	
ပ	7	35	7.6	204		N81164	Base substituted E.co	1.18e-03	
υ	80	32	6.9	91	σ	051746	Oligonucleotide probe	1.57e-02	
U	σ	27	5.8	89	32	T63255	Messenger RNA primer	1.00e+00	
O	10	27	5.8	68	33	T73397	Oligonucleotide tag c	1.00e+00	
υ	11	27	5.8	70	54	T14325	Conjugate formed by 1	1.00e+00	
ပ	12	27	5.8	7400	17	T09340	Tobacco mosaic virus	1.00e+00	
,	13	27	8	9789	24	T41852	CDNA encoding Plasmod	1.00e+00	
ีย	14	26	5.6	114	12	070467	Generic DNA sequence	2.25e+00	
	15	56	5.6	140	31	T76781	Staphylococcus aureus	2.25e+00	

15 25 5.4 64 24 141222 StabplyOcoccus and Section 25 5.4 68 27 7513397 StabplyOcoccus and Section 25 5.4 68 27 7513397 StabplyOcoccus and Sequence 4.96e+00 25 5.4 68 27 7513397 StabplyOcoccus and Sequence 4.96e+00 25 5.4 114 12 270472 StabplyOcoccus and Sequence 4.96e+00 25 5.4 114 12 270472 StabplyOcoccus and Sequence 4.96e+00 25 5.4 114 12 270472 StabplyOcoccus and Sequence 4.96e+00 25 5.4 114 12 270472 StabplyOcoccus and Sequence 4.96e+00 25 5.4 1175 270472 StabplyOcoccus and Sequence 4.96e+00 25 5.4 1175 270472 StabplyOcoccus and Sequence 4.96e+00 26 25 5.4 1175 270472 StabplyOcoccus and Sequence 4.96e+00 26 25 5.4 1175 270472 StabplyOcoccus and Sequence 4.96e+00 26 25 24 1175 270472 StabplyOcoccus and Sequence 4.96e+00 26 25 24 24 24 24 25 24 24	2000000000	2222222222	gdggggg	•	0;
16 25 5.6 24 21 175682 Staphylococcus au	24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1.088e+0 1.088e+0 1.088e+0 1.088e+0 1.088e+0 1.088e+0	e s trage -:	Gaps
16 26 5.6 240 31 176782 18 25 5.4 68 32 173325 21 25 5.4 68 33 173355 22 25 5.4 114 12 070465 23 25 5.4 114 12 070465 24 25 5.4 114 12 070465 25 5.4 114 12 070465 26 25 5.4 114 12 070465 27 25 5.4 114 12 070465 28 25 5.4 114 12 070465 29 25 5.4 114 12 070465 29 25 5.4 114 12 070465 29 25 5.4 1173 1 065185 29 25 5.4 1173 1 065185 29 25 5.4 1173 1 065185 29 25 5.4 1173 1 065185 29 25 5.4 1173 1 065185 29 25 5.4 1173 1 06648 41 24 5.2 114 12 070465 31 25 5.4 1582 2 171883 32 25 5.4 1584 2 172882 33 25 5.4 114 12 070465 34 25 5.4 1582 2 171883 35 25 5.4 1584 1 070465 36 24 5.2 1903 1 172882 37 24 5.2 1903 1 100648 42 24 5.2 1904 2 17888 44 24 5.2 1878 1 N90416 45 24 5.2 3001 1 006648 45 24 5.2 3001 1 006648 46 24 5.2 3001 1 006648 47 24 5.2 3001 1 006648 48 24 5.2 3007 3 7 758840 49 24 5.2 3007 3 7 758840 40 24 5.2 3001 1 006648 41 24 5.2 38077 27 758840 42 5.2 3007 3 7 758840 43 24 5.2 38077 27 758840 44 24 5.2 3001 1 006648 45 5.2 58077 27 758840 46 5.2 58077 27 758840 47 17752 48 5.2 58077 27 758840 48 5.2 58077 27 758840 49 5.2 58077 27 758840 40 6000000000000000000000000000000000		Tasming pwiscy used the property of the proper	uman G protein gamma tuman retinoid X rece NA sequence encoding rochloa panicoides C equence encoding a c tuman Factor XIII cod lasminogen gene from fuman polycystic kidn iycoplasma genitalium	glucocerebh therapy; er; ss. DL; lysosomal et ysosomal st HMG2 promo' ues, but is yt the proce hat induce lon systems systems systems and in systems and in systems of y of lysosod y of lysosod	32; Length 463; -198; 0; Indels 0
16 26 5. 18 25 5. 19 25 5. 20 25 5. 21 25 5. 22 25 5. 23 25 5. 24 25 5. 25 25 5. 26 25 5. 27 752, 41 24 5. 42 24 5. 43 25 5. 43 25 5. 44 24 5. 44 24 5. 45 24 5. 47 7752, 47 7752, 48 25 5. 48 25 5. 48 25 5. 48 25 5. 49 24 5. 41 24 5. 41 24 5. 42 24 5. 43 25 5. 44 24 5. 45 24 5. 46 24 5. 47 7752, 47 24 5. 48 24 5. 48 24 5. 48 24 5. 48 24 5. 48 24 5. 49 24 5. 48 24 5. 48 24 5. 49 24 5. 41 24 5. 41 24 5. 42 24 5. 43 24 5. 44 24 5. 45 24 5. 47 24 5. 48 24 6. 48 24 6				LIGNMENTS LIGNMENTS LITANSGENIC TOME; MEGA DN, Weiss DN, Weiss Lish. Treatmen Tish. The modified Treased pla Transg chee Tr	ore 463; ed. No. 1 ; Mismat
16 26 5. 18 25 5. 19 25 5. 20 25 5. 21 25 5. 22 25 5. 23 25 5. 24 25 5. 25 25 5. 26 25 5. 27 752, 41 24 5. 42 24 5. 43 25 5. 43 25 5. 44 24 5. 44 24 5. 45 24 5. 47 7752, 47 7752, 48 25 5. 48 25 5. 48 25 5. 48 25 5. 49 24 5. 41 24 5. 41 24 5. 42 24 5. 43 25 5. 44 24 5. 45 24 5. 46 24 5. 47 7752, 47 24 5. 48 24 5. 48 24 5. 48 24 5. 48 24 5. 48 24 5. 49 24 5. 48 24 5. 48 24 5. 49 24 5. 41 24 5. 41 24 5. 42 24 5. 43 24 5. 44 24 5. 45 24 5. 47 24 5. 48 24 6. 48 24 6	668 2 2 3 3 3 3 4 4 1 1 1 4 4 5 8 8 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	13 50 50 50 50 50 50 50 50 50 50 50 50 50	003 001 001 001 001 001 001 001 001 001	AA; 463 I = entry) lysosome = IUDA; INTER SY 3737. 3737. 3737. A Radd (K, Radd (K, Radd (K, Radd (M) INTER (T) 1752). Dn in uns matucally natically natically natically natically natically natically 111pp; Er (T71752). Novel R Novel R Nove	00.0% 00.0% ative
16 26 11 2 25 11 25 25 25 25 25 25 25 25 25 25 25 25 25	0 4 4 4 4 4 4 4 4	ਜ ••••••••••••••••••••••••••••••••••••	addaddadda 28	ndard; DD 7 (first ter. 9 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	larity Conse
SC ARRA	, , , , , , , , , , , , , , , , , , ,	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	444444444	1 CT-19 CT-19 CT-19 CT-19 CT-19 CT-19 CD-19 CG-1	latch cal S
SOCCOCCOCCATE TEACHER SERVICE SOCCOCCOCCATE SOCCOCCOCCATE SOCCOCCATE SOCCATE SOCCOCCATE SOCCOCCATE SOCCOCCATE SOCCOCCATE SOCCOCCATE SOCCATE SOCCOCCATE SOC	110 110 110 110 110 110 110 110 110 110	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	TI MANA SA	uery sest fatch
	0 0 0	O	0 00	SAUCHE WAY WAY TELEFORM WAY WANTED AND TO COOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOC	ᅜᄜᆇ

```
1109
                                                                                                179
                                                                                                                   929
                                                                                                                                                                      299
                                                                                                                                                                                                                                              417
                                                                                                                                                                                                                                                                                                                                                      heart failure; protein kinase;
                   caaatgcaaaatgtatgagttatttcataatagcccagttcgtatccaaatattttacac
                                                                                         atattattgtaaaagataatactccattcaaaatataaaatgaaaaaagtccagcggc
                                                                                                                                                              010572;
09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NYEB: ANP; BNP; CNP; kidney failure; heart fa:
hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                              /note= "GC and protien kinase activity"
Modified -site 24..26
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   Q10572 standard; DNA; 1047 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label- cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified -site 244..246
/label N 1919cos_site
Modified -site 277..279
/label N-919cos_site
/label N-919cos_site
/label N-919cos_site
Modified -site 349..351
/label N-919cos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 -site 161..163
N-glycos_site
1 -site 195..197
                                                                                                                                                                                                                                                                                                                                                                                                  /label= signal sequence
Protein 12
                                                                                                                                                                                                                                                                                                                                                                                                                              23..455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-glycos_site
1 -site 35..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label - N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                     /label- mature NPBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified -site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= N-glyco:
Modified -site
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9100292-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                            750
                                                                               810
                                                                                                                  870
                                                                                                                                    180
                                                                                                                                                     930
                                                                                                                                                                      240
                                                                                                                                                                                         990
                                                                                                                                                                                                          300
                                                                                                                                                                                                                           1050
                                                                                                                                                                                                                                             358
                                                                                                                                                                                                                                                               1110
                                                                                                                                                                                                                                                                                 418
                           Н
                                                             9
                                                                                                120
                                                                                                                                                                                                                                                                                                         셤
          음
                                         셤
                                                            δy
                                                                            셤
                                                                                               δ
                                                                                                            g
                                                                                                                                   ŏ
                                                                                                                                                   g
                                                                                                                                                                      Ω
                                                                                                                                                                                    ద
                                                                                                                                                                                                          δý
                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                          240
                                                                                                                          240
                                                                                                                                                              300
                                                                                                                                                                                                                                     420
9
                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig. 4a-4c; 110pp; English.

A 2.5 kb Ecori fragment of the HMGR gene (HMG2)-containing clone PTH295 was inserted into the Ecori site of Bluecript SK-vector to generate pDW101. A 1388 bp sequence from the 3' end of the 2.5 kb Ecori insert of pDW101 is given in 081473. This promoter region can be used to control gene expression in transgenic plants or cell cultures in response to wounding, elicitors, pest infestation,
         aaatgcaaaatgtatgagttatttcataatagcccagttcgtatccaaatattttacact
                                                                                                         tattattgtaaaagataatactccattcaaaatataaaatgaaaaagtccagcggca
                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 1388;
                                                                                                                                                                                                                                                                                                                                           HMG2; promoter; transgenic plant; post-harvest production; 3-hydroxy-3-methylglutaryl-CoA-reductase; HMGR; wounding; pathogen infection; pest infestation; inducible expression; pollen-specific expression; disease-resistance; pesticide-resistance; crop improvement; pDW101; ss. Lycoparshaon.esoulontum cv. VNNT Cherry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter expression systems - used for inducible prods. In plants and plant cell cultures, partic.
                                                                                                                                                                                                                                                    tttcctcaccggcggcagacttaccggtgaaagtaagcagstc 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 G;
                                                                                                                                                                                                                                                               ### TITCTTCACCGGCGGCAGACTTACCGGTGAAAGTAAGCAGSTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 4.13e-185;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VIRG ) VIRGINIA TECH INTELLECTUAL PROPERTIES.
Cramer CL, Welssenborn DL;
WPI; 95-081942/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 434;
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag- a
/note- "transcriptional start site"
TATA_signal 1003.1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.7%;
llarity 99.3%;
Conservative
                                                                                                                                                                                                                                                                                                .r 2
Q81473 standard; DNA; 1388
                                                                                                                                                                                                                                                                                                                          -SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
W09503690-A.
09-FEB-1995.
02-AUG-1994, U08722.
02-AUG-1993; US-100816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell cultures in respons
pathogen infection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1388 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 452; Conser
                                                                                                                                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 45
                                                                                                                                                                                                                                                                                                                                                                                                          misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                   61
                                                                     121
                                                                                      121
                                                                                                        181
                                                                                                                         181
                                                                                                                                           241
                                                                                                                                                            241
                                                                                                                                                                                               301
                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                      421
                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                   g
                å
                             유
                                                  ò
                                                                   ដ
                                                                                                                                          셤
                                                                                                                                                            ò
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                      ö
                                                                                 õ
                                                                                                                       'n
```

```
ntngday-mvvsgnngrngnrhannnarmananndavssnrnrh 948
                'label transmembrane domain
                                                                                                                                                                                                     Modified -site 277...279
Alabel N-glycos_site
Modified -site 349..351
Alabel N-glycos_site
Modified -site 600..602
                                                                                                                                                                           Modified -site 244..246
/label= N-glycos_site
Modified -site 277..279
                                                                                                                         ..163
                                                                                                                                     /label= N-glycos_site
4odified -site 195..197
                                                                                /label= N-glycos_site
Modified -site 35..37
                                                                                                          /label= N-glycos_site
Modified -site 161..1
                                                                                                                                                                'label N-glycos_site
                                                                                                                                                                                                                                                                     /label= N-glycos_site
WO9100292-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1047 BP;
                                                                                                                                                   Modified -site
                                                                   Modified -site
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q10324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   also be prepd
                                                                                                                                                                                                                                                                                                    10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                906
  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                   ä,
                                                                                                                                                                                                                                                                                                                            gvssnnnnrknmnnknnasmnwrnrwnnnnngnsnryhkgagsrntn-snrgssygsnmt 529
                                                                                                                                                                                                                                                                                                                                             308 AACCCGGTIGCCGCCGCGCTTTTTTTTTTTTTTTTTTTGAATGGAGTATTATCTTTTA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATAATATACTTTCTTTTTTTTTTTTTTTTGAAGTAAAGTTTTATATAGTCAAGTTG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 ACTGGTCAAGTGTAAAATATTTGGATACGAACTGGGCTATTATGAAATAACTCATACATT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             883
                                                                         Nationary Content receptor B - for diagnosis and treatment of Kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3: Fig 1: 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodm. Of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr—114,952). The protein (or variants) can be used in treatment of matriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can also be preped.
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                 530 ahgkynnnantghnkgnvvankhvnkkrnnntrnvnnnnkhmrdvnnnhntrnngacndn
                                                                                                                                                                                                                                                                                                                                                                                                                                       nnncnvtnycnrgsnndnnnndsnnndwmnrysnnndnvkgmannhnsnnsshgsnkssn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cvvdsrnvnkntdygnasnrstannddnnanyakknntannnnsgnnnnttgmnaadvys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 710 ngnnnnnanrsgnnynngndnsnknnvnkvrngnrnynrnsndrtnnnnnnvnnmnrcw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      770 andnanrndngnnkgnnrrnnknggtsnndnnnrmnnyannnnknvnnrtnaynnnkrk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 ITGCATTTGATAATTAGGTAATAATAGTTGAAAGTAGATATTAAATATTAAAATTT-GAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            830 anannynnnnhsvannnkrgntvnanandsvtnynsdnvgntansanstnmnvvtnnndn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     э;
                                                                                                                                                                                                                                                                       DB 2; Length 1047;
                                                                                                                                                                                                                                                                     h Similarity 9.6%; Score 45; DB 2; Length 1047 Similarity 9.6%; Pred. No. 1.47e-07; 41; Conservative 111; Mismatches 274; Indels
                                                                                                                                                                                                                                             51 T;
                                                                                                                                                                                                                                             83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- extracellular domain //Trote- "binds natriuretic peptides A,B and C]"
                                                                                                                                                                                                                                             15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q10572 standard; DNA; 1047 BP.
                                                                                                                                                                                                                                             87 A;
                                     Chang M, Goeddel D, Lowe D; WPI; 91-036711/05.
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 9.68;
22-JUN-1990; U03586.
23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide 1..22
/label- signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein 12
/label= mature NPBR
                                                                                                                                                                                                                                            1047 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                890 ytcndannd 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 ATCGTATTG 1
                                                                  N-PSDB; 010324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
                                                                                                                                                                                                                                                                                                                           471
                                                                                                                                                                                                                                                                                                                                                       427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT

ID 01

DD 01

DD 09

DD HU

NW NP

NW NP

NO NP

NP NP NP

FT 7 7

FT 7 7

FT 7 7
 C.
                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                    ç
                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                               S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          გ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
240 ATATTATTGTAAAAGATAATACTCCATTCAAAATATAAAATG-AAAAAGTCCAGCGGG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nrrnnknggtsnndnnnrmnnyannnnknvnnrtnaynnnkrkanannynnnnhsvann 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nkrgntvnanandsvtnynsdnvgntansanstnmnvvtnnndnytcndanndnndvykv 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vvankhvnkkrnnntrnvnnnnkhmrdvnnnhntrnngacndnnnncnvtnycnrgsnnd 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nnnndsnnndwmn-rysnnndnvkgmannhnsnnsshgsnkssncvvdsrnvnkntdygn 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 CAAATGCAAAATGTATGAGTTATTTCATAATAGCCCCAGTTCGTATCCAAATATTTTACAC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 CAACCGGGTTCCTATAAATACATTTCCTACATCTTCTTCTTCTCCTCACATCCCATCACTC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of matriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nngndnsnknnvnkvrngnrnynrnsndrtnnnnnnnvnnmnrcwandnanrndngnnkgn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asnrstannddnnanyakknntannnnsgnnnnttgmnaadvysngnnnnnanrsgnny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.1%; Score 42; DB 2; Lenc
larity 8.4%; Pred. No. 2.29e-06;
Conservative 109; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 G;
                                                         rote= "GC and protien kinase activity" dodified -site 24..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
Jomain 479..1047
/label= cytoplasmic domain
```

э; Э

ö

Gaps

ö

ö

ø

/*tag=

```
Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 bnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhn-hnncncccbn 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an Oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NoV-1990 (first entry) asse subha-fragment. Base substituted E.coli beta-galactosidase alpha-fragment. E.coli beta galactosidase alpha-fragment; base substitutions; ss. Escherichia coli.
                                                                                                                                                                                                                                                                                                8 gcgssvhsyyvvhvvshhhsvhhvvhhvhvhvvhhvhhvhyhvyvsv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q51746 standard; cDNA; 91 BP.
Q51746;
31-MAY-1994 (first entry)
Oligonuclectide probe MK14-A
Oligonuclectide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                              Score 35; DB 9; Length b., Pred. No. 1.18e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.18e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 nhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 ATAATTGTTAAAAGAAGAGGGGGGGAT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/function=multiple cloning site
                                                                                                                                                                                                                                                                                                                                                                                                              N81164 standard; DNA; 204 BP
                                                                                                                                                                  7.6%;
larity 5.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1988; 105163.
03-APR-1987; US-034819.
                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP-285123-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
ID Q5
AC Q5
DT 31
DE O1
KW O1
                                                                                                                                                                                                                                                                                                                                                                                      RESULT
    8888888
                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUSO) SUOWEN SOKERI OY.

Lehtovaara P. Knowles J, Koivula A, Bamford J, Reinikainen T;

WPI: 88-279927/40.

Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -

By prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of
E.coil beta-galactosidase. The wild type sequence was obtained as a
E.coil beta-galactosidase. The wild type sequence was obtained as a
E.coil beta-galactosidase. The wild type sequence as obtained as a
E.coil beta-galactions within a specified region. The
possible nucleotide positions within a specified region. The
contained is and generated in this way are used as primers for
reverse transcriptase. Nucleotides are misincorporated by the
transcriptase and the molecules are completed to forms that can be
camplified and then expressed in a suitable host-vector system.
The sequence covers all 176 difft base substitutions, most of which
cocurred singularly in any given mutant.

See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 gymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvk-ydccynachhddhyvybbbvy 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 GTTATTTCATAATAGCCCAGTTCGTATCCAAATATTTTACACTTGACCAGTCAACTTGAC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                  Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligo nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 5.66e-06;
55; Mismatches 34; Indels
419 TTTTCCTCACCGCGGCAGACTTACCGGTGAAAGTAAGCAGST 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 nvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 TATATAAAACTTTACTTCAAAAATTAAAAAAAAAAAGAAGT 239
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                            /function-multiple cloning site
primer_bind 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 14; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .r 6
Q51746 standard; cDNA; 91 BP.
Q51746;
                                                                       T 5
N81164 standard; DNA; 204 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BECT ) BECTON DICKINSON CO. Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 11.8%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.98;
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1987; US-034819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1993; 108325.
26-MAY-1992; US-889651
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1988; 105163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-378844/48
                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                misc_feature
                                                                                                                   N81164;
<del>98--</del>NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-571911-A.
01-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                      EP-285123-A.
                                                                                                                                                                                                                                                                                                                                       primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
```

Query Match

요 ò ð

ದ

ä

Gaps

Shank DD,

RESULT
AC 005
AC

sambles

108 Others;

```
Sorting poly:nuclectide(s) on to solid supports by attachment to oligo:nuclectide tags - then specific hybridisation of tags to immobilised complement, e.g. for automated DNA mapping and sequencing, genetic identification and diagnosis bisclosure; Page 22; 79pp; English.

A method of sorting a population of polynuclectides on to one or more solid supports has been produced. The polynuclectides are sorted on to solid supports by: (a) attaching an oligonuclectide tag to each polynuclectide, each tag being minimally cross-hybridising; (b) sampling the population so that all different polynuclectides have different tags; (c) sorting by specific hybridisation of the tags with their complements which are attached as uniform populations of identical oligonuclectides in spatially distinct regions on one or more solid
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phase support. The present sequence represents a primer, from a set, preferably containing complements of tag sequences. When the population of polynucleotides consists of messenger RNA, oligonucleotide tags may be attached by reverse transcribing the mRNA with the set of primers including the present sequence. The method can be used to identify a population of mRNA molecules; to detect presence/absence of selected target sequences in a target polynucleotides; or to identify polynucleotides, including new ones in cDNA libraries, e.g. for construction and use of combinatorial chemical libraries; large scale DNA mapping and sequencing; genetic identification; medical diagnosis (e.g. analysis of gene expression in diseased and normal tissue). The
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-0CT-1997 (first entry)
Messenger RNA primer containing a complement tag sequence.
mRNA; oligonucleotide tag; hybridisation; automated DNA mapping;
genetic identification; polynucleotide; target; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                 Claim 3; Page 14; 23pp; English.
Oligonuclectide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may
                                                                                                                                                                          New oligo:nucleotide probes specific for Mycobacteria – used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                               be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 CCGCCGGTGAGGAAAAAGGGAGAAAAAGTGTTGTTGTGGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 yvvhvvshhhsvhhvvhhvhvsvvvhhvvhhvhyhvyvsv 60
                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 9; L/
Pred. No. 1.57e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "5'-labelled with biotin"
WO9641011-A1.
                                                                         24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                             6.9%;
ilarity 0.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
ID T63255 standard; DNA; 68 BP.
AC T63255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995; US-478238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1995; WO-U12791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SPEC-) SPECTRAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brenner S;
                                                                                                                                     Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97-099943/09.
                                                                                                                                                     WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                       01-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                     Shank DD,
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 5
                                                                                                                                                                                                                     samples
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
S
```

```
Massively parallel signature sequencing - useful to test toxicity of massively parallel signature sequencing - useful to test toxicity of compound, or to identify genes which are differentially expressed in presented tissue or a test animal after treatment with a compound bisclosure; Page 26; 65pp; English.

CC T73397-T73400 represent amplification primers that can be used in the method the invention. The method is for determining the toxicity of a compound. The method comprises administering a compound to a test compound. The method comprises from each mRNA population Each CDNA molecules from each mRNA population of compounds. The method an oligonous leads are then sorted by completel by a statished an oligonous leads are then sorted by completel is then sampled. The cDNA molecules are then sorted by completel is specifically hybridising the tags with their complements, which are attached in spatially discrete regions on lor more solid phase supports. The generoy distribution of expressed genes for each tissue: The frequency of the compound. The method, which comprises the massively parallel compound, or to identify genes which are differentially expressed in a selected tissue of a test animal after treatment with a compound, in a compound, or to identify genes which are differentially expressed in a selected tissue of a test animal after treatment with a compound, in a may also be used to fingerprint mRNA populations, either in isolated may also be used to fingerprint mRNA populations, either in isolated may also be used to fingerprint mRNA populations, either in isolated may also be used to fingerprint and sequence information is obtained from a large sample, e.g. 10 to the found of the compound of the compound.
method is easily automated for manipulation and sorting of polynucleotides in large scale parallel processing where many target polynucleotides, or many target segments of a single polynucleotide, are sequenced simultaneously.

8 4 6; 21 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-DEC-1997 (first entry) objective of the content 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100000, or more, of cDNA attached to separate microparticles. Sequence 68 BP; 3 A; 13 C; 4 G; 21 T;
                                                                                                                                                                                                                                                                                       Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 68;
                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 www.www.www.www.www.www.ggtttttttttttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 27; DB 33; Len
21.1%; Pred. No. 1.00e+00;
                                                                                                                                                                                                                                                                                  Score 27; DB 32; Pred. No. 1.00e+00;
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1995; WO-U12791.
(LYNX-) LYNX THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I 10
T73397 standard; DNA; 68 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "oligonucleotide tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 31.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "biotin labelled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO-U09513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-1996; U16342
06-JUN-1996; WO-U099
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 14; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97-235911/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9713877-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martin DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
    Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
/transl_except= ATA encodes Tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T41852 standard; DNA; 9789 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= g
/transl_except= AAT encodes
misc_feature 6257..6259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 5.8%;
Local Similarity 72.9%;
                                               3214..5031
                                                                                               5032..6600
                                                                                                                                                   6601..6933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2909..2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3461..3463
                                                                                                                                                                                                                                                                                               16-JUN-1995; U07754.
17-JUN-1994; US-261663.
(REGC ) UNIV CALIFORNIA.
(USDA ) US SEC OF AGRIC.
Baker BJ. Whitham SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/transl except= ATT
                                                                                                                                                                                                                                                                                                                                                                                                         Baker BJ, Whitham WPI; 96-058144/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_except=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= f
'transl_except=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= e
transl_except=
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; R88122
                                                                                                                                                                                                                                /*tag= i
WO9535024-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                  28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                           /*tag=
exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                       *tag=
                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                            *tag=
                                                    ntron
                                                                                                                                                      ntron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLT SOLVE SO
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fingerprinting

Disclosure; Page 20; 71pp; English.

Disclosure; Page 20; 71pp; English.

Cover T; (b) attaching an oligonucleotide tag from a repertoric of tags, to each fragment such that all the same fragments have the same tag, to each fragments such that all the same fragments have the same tag, and all different fragments have different tags; (c) same tag, and all different fragments have different tags; (c) cacho of the fragments; and (e) determining (1) of a portion of each of the fragments; and (e) determining (1) of a portion of each of the fragments. The tagging system can be used with the sequences of the fragments. The tagging system can be used with single base sequencing methods to sequence polynucleotides up to several Kilobases in length. The tagging system permits many come or more solid phase supports and sequenced simultaneously.

A preimer which is initially used to reverse transcribe mRNA is described in T14322. If the amplified product is then needed to be attached to a solid phase support a sequence like the one given in T14323 may be used. The mRNA would then be removed and the second strand of cond or conjugate would have a formula similar to this.

Sequence 70 BP; 2 A; 12 C; 3 G; 19 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 96-222023/22.
Labelling and sorting mols. using oligo:nucleotide tags - useful in
large-scale parallel operations, e.g. DNA sequencing and mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                       16-7AN-1997 (first entry)
Conjugate formed by labelling and sorting of nucleotide molecules.
Labelling; sorting; sequencing; tag; tagging; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-1996 (first entry)
Tobacco mosaic virus resistance N gene.
Tobacco mosaic virus resistance; TMV; N gene; Solanaceae; crop improvement; transgenic plant; crop improvement; ds. Nicotiana glutinosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 www.www.www.www.www.www.ww.wgttttttttt 58 ::::|::: : :::|::: !||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 24;
Pred. No. 1.00e+00;
22; Mismatches 9
                                                                                                                                                                                                                                                                     /note= "This N represents the amplified cDNA
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 12
T09340 standard; DNA; 7400 BP.
                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-1994; US-322348.
19-DECT-1994; US-359295.
(LYNX-) LYNX THERAPEUTICS INC.
Brenner S;
                  T 11
T14325 standard; DNA; 70 BP
T14325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sebect-Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .003..2098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2099..2940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        773..1002
                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1995; U12678.
                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                  sequence"
WO9612039-A1.
                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                          25-APR-1996
                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,T09340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag-
intron
/*tag-
```

RESCRIPTION OF SECULAR AND SECULAR SET TERMS AND SECULAR SECUL

```
3645 atattttatcgtaattttttaaaaatttgtcaaataatgcaaatgaaaaattaaatttt 3703
Plant virus resistance gene N sequences from tobacco - useful for generating transgenic Solanaceous plants resistant to Tobacco Mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 52-60; 98pp; English.

The N gene (T09341) of Nicotiana glutinosa codes for a protein (R88123) that mediates resistance to tobacco mosaic virus (TMV). The gene was isolated from a genomic library of N. glutinosa by screening using a cDNA clone. The N gene can be used to generate transgenic plants, esp. Solanaceae, resistant to TMV, or as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-1997 (first entry)
CDNA encoding Plasmodium falciparum erythrocyte membrane protein.
Plasmodium falciparum; erythrocyte membrane protein; malaria;
detection; identification; treatment; prevention; parasite; ss.
Plasmodium falciparum MC type.
                                                                                                                                                                                                                                                                                                        2512 T;
                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 17; Length 7400; Pred. No. 1.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                        1246 G;
                                                                                                                                                                                                                                                                                                     1147 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC encodes Aspartic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= Erythrocyte membrane protein misc_feature 518..520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAA encodes Glutamine
5546..5548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_except= GTA encodes Tyrosine misc_feature 656..658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCT encodes Arginine 6254..6256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 326..9497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encodes Leucine
                                                                                                                                                                                                                                                                   probe to isolate homologous genes.
Sequence 7400 BP; 2495 A;
```

ő

```
T000D
                                                                                                                                                                                            P-PSDB; R65153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gillespie D;
WO9418318-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 110 111 110 111 110 111 110 111 110 111 110 111 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110 110
  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ဥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malaria parasite infections

Disclosure; Figure 12; 149pp; English.

Disclosure; Figure 12; 149pp; English.

Chaptypeptide comprising a Plasmodium falciparum (Pf) erythrocyte

Chaptypeptide comprising a Plasmodium falciparum (Pf) erythrocyte

malaria parasite infection. The polypeptides can inhibit, block or

reverse the sequestration of erythrocytes in patients suffering from

malaria. Nucleic acids derived from the PfEMP1 gene can be used as

primers used to generate characteristic amplification patterns from

different P. falciparum strains. Antibodies specifically

immunoreactive with the PfEMP1 polypeptide or its fragments may be

cused in diagnosis of malaria infection. This sequence encodes the

PfEMP1 protein of the MC type of Plasmodium falciparum. An

alternative, truncated version of the coding sequence (a CDNA clone)

is given in T41853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8135 ataaaaaaaaaaaatttaaaaaaatgttaaaaaaaaatatatatatatatatataaaaa 8194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 ATATAAAACTITACTICAAAAATTAAAAAAAAAAAAGAAGTATATTATTGTAAAAGATAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generic DNA sequence to generate a random TSAR petide library.

TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 31; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Plasmodium falciparum erythrocyte membrane proteins - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2498 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  develop products for the diagnosis, treatment or prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1837 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 24;
Pred. No. 1.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "this sequence represents 'Z'; Z can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1393 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8195 aaaaataaaaaaaatgtaaaaaaaaaaa 8223
                                                                                                    TTC encodes Isoleucine 6272..6274
                                                                                                                                                                                                                                    ATT encodes Asparagine 6278..6280
                                                                                                                                                                                                                                                                                                   /transl_except= GGA encodes Tryptophan intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 TACTCCATTCAAAATATAAAATGAAAAAA 287
                                                                                                                                                                 transl_except= ATA encodes Histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baruch DI, Howard RJ, Pasloske BL; WPI; 96-497376/49. P-PSDB; W00384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                      AAC encodes Lysine
6269..6271
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AFFY-) AFFYMAX TECHNOLOGIES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4061 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q70467 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.8%;
Best Local Similarity 65.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1995 (first entry)
6263..6265
                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1996; U05798.
27-APR-1995; US-430908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55..60
                                                                                  '*tag= j
'transl_except= TTC
                                                                                                                                                                                                                                    /transl_except- ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9789 BP;
                                   transl_except=
                                                                                                                                                                                   isc feature
                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                 WO9633736-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
misc_feature
                                                              misc_feature
                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                        31-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            070467;
                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT

ID 07

AC 07

OD 05

DE G6

KW CFW TS

KW CFW CFW

FFT MI

FFT MI

FFT MI

FFT CO
å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
PPERDIX R65153

Identifying proteins or peptide(s) which bind a ligand - by
Identifying proteins or peptide(s) which bind a ligand - by
Screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
Disclosure: Page 35; 255pp; English.

COM67 is a generic DNA Sequence used to generate random TSAR (Totally
COM67 is a generic DNA Sequence used to generate candom TSAR (Totally
COM67 is a generic DNA Sequence state shown in Synthetic Affinity Reagents) peptides. This generic formula can also be
crepresented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1Y. X
and Y are flanking restriction sites (X is not the same as Y) that are
contributed as follows: X(NNB)16(TGC)(NNB)12(NNB)11Y. X
and Y are flanking restriction sites (X is not the same as Y) that are
comprising at least two functional regions - a binding domain with
Affinity for a ligand and a second effector peptide portion that is
comprising at least two functional regions - a binding domain with
affinity for a ligand and a second effector peptide portion that is
commically or biologically active. They may further comprise a linker
comprising the unpredicted or variant residues. These residues
confer some degree of conformational rigidity to the peptides. The TGARS
confer some degree of conformational rigidity to the peptides. The TGARS
or comprising a TSAR binding domain can be used in vivo to
deliver a chemically or biologically active modety, eg. metal ion,
cell. They can also replace the function of macromolecules, eg.
complex methods of hybridoma formation or in vivo antibody production.
The TSARs are easily characterised and have designed activity allowing
direct and rapid detection in a screening process.
2 T;
2 Cg. 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asymmetric polymerase chain reaction
Example 1; Column 6; 9pp; English.
In a specific example of a novel process for amplifying an amount
(known or unknown) of a double-stranded nucleic acid segment to produce single-stranded nucleic acid in an amount that is proportional to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 GCGCTGGACTTTTTTCATTTTATATTTTGAATGGAGTATTATCTTTTACAATAATATACT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-1997 (first entry)
Staphylococcus aureus exfoliative toxin A gene capture probe.
Asymmetric polymerase chain reaction; nucleic acid amplification;
PCR: detection; assay: exfoliative toxin A; ETA; skin lesion;
competitive primer; capture probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quantitative nucleic acid amplification - by competitor primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 12; Length 114
Pred. No. 2.25e+00;
28; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 TICTITITITITAATITITIGAAGTAAAGTITITATATAGTCAAGTIG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176781 standard; DNA; 140 BP
                                                                            31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 3.7%;
Matches 4; Conservative
                                             US-176500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1996; 628417.
05-APR-1996; US-628417.
US-013416
                                                                                                                                                                                                           WPI; 94-279739/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97-271311/24
```

```
starting amount of the nucleic acid, the Staphylococcus aureus

exfoliative toxin A (ETA) gene was used as the DNA template. The

region comprising nucleotides 165-436 was amplified by symmetric,
asymmetric or competitor primer asymmetric PCR, the

mount of primer ETA-B was reduced and for competitor primer
asymmetric PCR a competitor primer ETA-B2 (see T76780) was added

with upstream primer ETA-A2 after the initial cycling reaction. PCR

products containing ETA-Specific sequences were detected

radioactively by a capture system which employed a bifunctional

capture probe ETA-CP (see T76781 and T76782). ETA-CP was designed

capture probe ETA-CP (see T76781 and T76782). ETA-CP was designed

coapture the amplified sense strand onto capture membranes

to capture the amplified sense strand onto capture membranes

complementary to nucleotides 313-360 of the ETA gene and through hybridisation

membranes. A radioactively labelled "label probe" (see T76783),

complementary to nucleotides 389-410 of the ETA gene was used to

detect the amplicons. Results showed that hybridisation of the

capture probe and label probe to the denatured symmetric PCR

prider tranded PCR products of the asymmetric and competitor

primer asymmetric reactions.

Sequence 140 BP; 121 A; 3 C; 4 G; 12 T;
   8888888888888888
```

ö 0; Gaps Length 140; Score 26; DB 31; Length 140; Pred. No. 2.25e+00; 0; Mismatches 32; Indels Query Match 5.6%; Best Local Similarity 64.4%; Matches 58; Conservative

윱 ò

84 аававававававававававававава 113

g ö

258 ATACTCCATTCAAATATAAAATGAAAAA 287

Search completed: Tue Feb 3 19:49:21 1998 Job time: 272 secs.

US-08-713-928A-5.rsta

ì

**************************************	**************************************
MPsrch_nn n.a	n.a. database search, using Smith-Waterman algorithm
n on: Tabular output not	ue Feb 3 19:49:46 1998; MasPar time 258.59 Seconds 884.200 Million cell updates/sec
Title: >US. Description: (1-4) Perfect Score: 463 N.A. Sequence: Comp:	S-08-713-928A-5 -463) from USO8713928A.seq 3 1 CAATACGATATTACCGAATACCGGTGAAAGTAAGCAGSTC 463 GITATGCTATAATGGCTTATGGCCACTTTCATTCGTCWAG
Scoring table: TAB	ABLE default ap 6
Nmatch STD : Dba	ase 0; Query 0
Searched: 66	5703 seqs, 246912890 bases x 2
Post-processing: Mi	nimum Match 0% sting first 45 summaries
Database: ES	EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:E EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 :EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST2 :EST31 22:EST22 23:EST23 24:EST24 25:EST25 26:EST2 :EST37 20:EST22 23:EST23 24:EST24 25:EST25 26:EST2
	EST33 44:EST34 35:EST43 30:EST33 31:EST31 32:EST33 EST33 34:EST33 34:EST35 36:EST36 37:EST31 32:EST33 EST33 34:EST34 35:EST35 36:EST36 37:EST33 40:EST40 41:EST41 42:EST42 43:EST43 44:EST45 EST34 64:EST46 49:EST49 50:EST35 EST35 54:EST35 54:EST35 55:EST35 56:EST35 54:EST36 65:EST55 56:EST55 56:EST55 56:EST55 56:EST55 56:EST55 56:EST56 65:EST66 62:EST66
r Datahaso	SST63 64:EST64 65:EST65 66:EST6 SST69 70:EST70 71:EST71 72:EST7 SST81 82:EST82 83:EST83 84:EST8 SST87 88:EST88 89:EST89 90:EST9 SST93 94:EST94 95:EST95 96:EST9
	EST199 100:EST100 101:EST101 102:EST102 103:EST103 :EST104 105:EST105 106:EST106 107:EST107 108:EST10
	EST124 125:EST125 126:EST126 127:EST127 128:EST12 EST129 130:EST130 131:EST131 132:EST132 133:EST13 EST134 135:EST135 136:EST136 137:EST137 138:EST13 EST139 140:EST141 141:EST141 142:EST142 143:EST14
	14 143:ES1143 140:E 54 150:ES1150 151:E 59 160:ES7160 161:E 64 165:ES7165 166:E 64 175:ES7170 171:E 74 175:ES7173 176:E

```
yy30d11.51 Soares fet 5.13e-05
yg32h08.51 Homo sapie 1.40e-03
mh212h2.11 Soares mou 1.40e-03
mh213b08.11 Life Tech 6.98e-03
o742c3 Plasmodium fal 6.98e-03
ana13b12.71 Beddington 6.98e-03
ana2f11.71 Beddington 3.36e-02
xb32d06.51 Homo sapie 3.36e-02
yf1f1f1.51 Homo sapie 3.36e-02
yf1ff1.51 Homo sapie 3.36e-02
yg53g12.74 Homo sapie 3.36e-02
yg53g12.74 Homo sapie 3.36e-02
yg53g12.74 Homo sapie 3.36e-02
yg53g12.71 Homo sapie 3.36e-02
yg58g10.51 Homo sapie 3.36e-02
yg78fd10.51 Homo sapie 3.36e-02
cXb2-218T Homo sapie 3.36e-02
cXb2-218T Homo sapie 1.56e-01
yg02h06.x1 Soares mou 1.56e-01
yg02h06.x1 Soares mou 1.56e-01
yg02h06.x1 Soares mou 1.56e-01
yg02h06.x1 Homo sapie 1.56e-01
yg02h06.x1 Soares mou 1.56e-01
yg02h06.x1 Homo sapie 1.56e-01
yg02h06.x1 Soares mou 1.56e-01
yg2ad08.71 Homo sapie 1.56e-01
yg2ad08.71 Homo sapie 1.56e-01
yg2ad08.71 Homo sapie 1.56e-01
xg13ay qmbPfH3.1, G. 1.56e-01
yi23a08.71 Homo sapie 1.56e-01
c26c01.x1 Soares mou 1.56e-01
xd20e01.x1 Soares mou 1.56e-01
zc26c01.x1 Soares mou 1.56e-01
zc26c01.x1 Soares mou 1.56e-01
zc26c01.x1 Soares mou 1.56e-01
zc26c01.x1 Soares mou 1.56e-01
zc3g3g1.x1 Soares mou 1.56e-01
zc43g07.x1 Homo sapie 1.56e-01
zc43g07.x1 Soares mou 1.56e-01
zc43g10.x1 Soares mou 1.56e-01
zc43g10.x1 Soares mou 1.56e-01
zc44g10.x1 Soares mou 1.56e-01
zc44g10.x1 Homo sapie 1.56e-01
ym29b05.x1 Homo sapie 1.56e-01
                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
183:EST183
188:EST188
193:EST193
179:EST179 180:EST180 181:EST181 182:EST182 184:EST184 185:EST185 186:EST186 187:EST187 188:EST189 190:EST190 191:EST191 192:EST192 194:EST194 195:EST195 196:EST196
                                   Variance 4.238; scale 2.554
                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                           HSCOHG121
N98059
                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                         ATTS1181
R42498
AA184945
H82133
R65859
N97347
                                                                                                                                                                                                                                                                                                                                                       T02659
AA185015
W45543
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                   AA072359
AA153231
T18158
                                                                                                                                                                                                                                                W82081
AA141823
T23157
                                                                                                                                                                                                                                                                     AA143490
AA117240
T02709
                                                                                                                                                                                                                      AA214473
AA099054
                                                                                                                                                                                                                                                                                                                                                                                    W46716
W58509
AA032099
AA164955
W49719
                                                                                                                                                                            AA104461
                                                                                                                                                                                                 AA034637
                                                                                                                                                                                                               AA184881
                                                                                                               N51049
                                                                                                 H
                                                                                                                                                                                   114
1188
1176
1176
1183
1192
                                                                                                                                                                                                                                                                      1199
1150
1150
1150
1150
1150
1150
                                                                                                                                                       192
146
99
                                                                                                  DB
                                   Mean 10.824;
                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                           Score
                                                                                                               Statistics:
                                                                                          Result
No.
                                                                                                                                                 υυυ
                                                                                                                                                 υυ
                                                                                                                                                                      O
                                                                                                                                                                                           O
                                                                                                                                                                                                                                                                                    000
                                                                                                                                                                                                                                                                                                                                                                       O
                                                                                                                                                                                                                                                                                                                                                                                            O
                                                                                                                                                                                                                                                                                                                                                                                                                υ
```

N51049 418 bp mRNA EST 28-JAN-1997 yv30041:s1 Soares fetal liver spleen lNFLS Homo sapiens CDNA clone 244245 3' similar to contains Alu repetitive element; contains L1.t2 L1 repetitive element; .
N51049 91192215

RESULT 1 LOCUS DEFINITION

ACCESSION NID KEYWORDS

```
1..365
                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 a
                                                                                                                                                                                     Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91282657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W08634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                   REFERENCE
                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 740 forward
Seq primer: ml3 -40 forward
High quality sequence stop: 337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human clone=34206 library-Soares infant brain lNIB vector-Lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 418) 110 418 11114er,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 183; Length 418;
Pred. No. 5.13e-05;
0; Mismatches 27; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructed by Bento Soares and M.Fatima Bonaldo." /clone="244245" /clone="124245" /clone_1ib="Soares fetal liver spleen lNFLS" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="20 week-post conception fetus"
/lab_nost="DH10B (ampicillin resistant)"
complement(<1...418)
67 c 87 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 ttttttttttgagatgaggtcttgtttgt 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 TITAATTTTTGAAGTAAAGTTTTATATAGT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.5%;
Best Local Similarity 69.2%;
Matches 63; Conservative
                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESOUR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
             ORGANISM
                                                                                                                                              TITLE
                                                                 REFERENCE
                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                COMMENT
SOURCE
```

g

```
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schollenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 365)
Hillier, C. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO8634 479 bp mRNA EST 05-SEP-1996
mb42b12.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 332063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashUrMerck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB 26; Length 365
Pred. No. 1.40e-03;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 IIICTITITITITIAAITITITGAAGTAAAGITATAAAGI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ttttttttttttttaactttttcaagtaatgttatgtacagt 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
High quality sequence stops: 240
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 g
                                                                                                                                                                                                                                                                                                                                 The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="34206"
56 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.0%;
Best Local Similarity 83.3%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                   G00-406-553
```

```
/dev_stage="7.5dpc"
/lab_host="DH125"
<1..>205
     /strain="C57BL/6J"
                                                                                                                                                                                                                Query Match 5.8%;
Best Local Similarity 81.4%;
                                                                                                                                                               30 C
                                                                                                                                                                                                                                                   35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AA153231
91724900
                                                                                                                                                                                                                                                                                                                                                                              ഹ
                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                            MRNA
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                          ô
                                                                                                  1 (bases 1 to 175)
Marra M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marra M., Hullier, L., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA072359 175 bp mRNA EST 02-OCT-1996 mf13b08.rl Life Tech mouse brain Mus musculus cDNA clone 404919 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:248687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 TITITICATITITATATITICAAIGGAGTATTATCTITIACAATAATATACTITITITI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 479
                                                                                                                                                                                                                                                                                                      /clone="332063"
/clone="332063"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (amplcillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                    Drw.Minoru Ko (Wayne State University).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 124;
Pred. No. 1.40e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: -28M13 rev1 from Amersham
High quality sequence stop: 134.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              334 t
                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Mus musculus"
            Seq primer: ETPrimer
High quality sequence stop: 477.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                              0
9
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.0%;
Best Local Similarity 56.3%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 tttnnttttt 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 TITAATITIT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse
MGI:213463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA072359
91590720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus.
                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                            MRNA
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
```

g

Cb

ద g

```
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL6 x DBA"
/note="Vector: pCMV-SPORT; Site_1: Sall; Site_2: Notl;
/note="Vector: pcm of sall; Site_2: pcm of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
/note="Vector: pCMV-SPORT2; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. pCMV-SPORT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA153231 205 bp mRNA EST 11-DEC-1996 mn31b12.rl Beddington mouse embryonic region Mus musculus cDNA clone 539519 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Beddington mouse embryonic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector."
/clone="404919"
/clone_lib="Life Tech mouse brain"
/dev stage="adult"
/lab_host="DH10B"
<1..>175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 6.98e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative full length read vector to vector length is 659 Seq primer: -40ml3 ET High quality sequence stop: 128. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                               20 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="539519"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="pooled"
```

BASE COUNT

ORIGIN

26

셤 ð

γò

φ

RESULT

DEFINITION

CCESSION

WORDS

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

```
Aarra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40Ml3 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL17266 236 bp mRNA EST 15-NOV-1996
mn22f11.r1 Beddington mouse embryonic region Mus musculus CDNA
clone 538701 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 405) Hollaes. L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevsskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Stratagene lung carcinoma 937218"
/dev_stage="cell line NCI-H69"
/lab_nost="SOLR (kanamycin resistant)"
complement(<1...>405)
83 c 66 9 165 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 192; Length 405;
Pred. No. 6.98e-03;
0; Mismatches 34; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 attttattttatttattttattttattttaaattt 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 TAATTTTTGAAGTAAAGTTTTATATAGTCAAGTT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
  element L1 repetitive element ;. AA135806
91696817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 383
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="565719"
                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%;
llarity 64.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..405
                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 61; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91672484
                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA135806 405 bp mRNA EST 30-NOV-1996 zn93b08.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 565719 3' similar to contains Alu repetitive element; contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                malaria parasite clone-0742c library-czapPFDd2.1, Debopam Chakrabari strain-Dd2 vector-Lambda ZAP II host-E. coli XL-1 blue primer-T3 Rsitel-EcoR I Rsite2-kno I PolyA+ RNA, from asynchronous blood stage parasites of the Dd2 isolate cultured in vitro, was reverse transcribed using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into EcoR I + Xho I digested lambda ZAP II
                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eucaryotae; Protozoa; Apicomplexa; Sporozoa; Coccidia; Eucoccidida; Haemosporina; Plasmodium.

(Dases 1 to 265)
Chakrabarti,D., Reddy,G.R., Dame,J.B., Almira,E.C., Laipis,P.J., Farl,R.J., Yang,T.P., Rowe,T.C. and Schuster,S.M.
Analysis of Expressed Sequence Tags from Plasmodium Falciparum Mol. Biochem. Parasitol. 66, 97-104 (1994)
                                                                                                                                                 30-AUG-1994
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                          ó
                                                                 Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 29; Indels
                                                                                                        0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                            T18158 265 bp mRNA EST
0742c3 Plasmodium falciparum cDNA clone 0742c 5'
462944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Plasmodium falciparum"
                                                               DB 170;
6.98e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 17;
Pred. No. 6.98e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Debopam Chakrabarti
Biotechnology & Infectious Diseases
University of Florida
Box 110880, Gainesville, Fl 32611
Tel: 9043924700 ext. 5817
Fax: 9043929704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111
23
                                                                 Score 27;
Pred. No.
                                                                                                                                                                                                                                  116 aaaaaaaaaaaaaaaaaaaaaaaaa 144
                                                                                                                                                                                                                                                                           259 TACTCCATTCAAATATAAAATGAAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dchak@icbr.ifas.ufl.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attttttgcacacatattttacat 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="0742c"/strain="Dd2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.8%;
Best Local Similarity 65.9%;
Matches 56; Conservative
                                                            Query Match
Best Local Similarity 65.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 c
  O
1
  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Bioc
95075403
160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
```

ö

ö

source

BASE COUNT

ORIGIN

LOCUS DEFINITION

RESULT

72

ŝ

Сp

```
Query Match 5.6%;
Best Local Similarity 68.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 C
                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                                                                                                                    Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1..>255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:338241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91650638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL6 x DBA"
/note="Vector: pCMV-SPORT; Site_1: Sall; Site_2: Notl;
/note="Vector: pCMV-SPORT; Site_1: Sall; Salt; Sal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 255)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2532406.s1 Homo sapiens cDNA clone 305291 3' similar to contains element PTR5 repetitive element;
                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Beddington mouse embryonic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 146; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 13; Indels
                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26; DB 146;
Pred. No. 3.36e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 t
                           Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 228.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="pooled"
/dev_stage="7.5dpc"
/lab_host="DH12s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="538701"
                                                                                                                                                                                                                                                                                                                                                                                                   MGI:325637
Seq primer: -40ml3 ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.6%;
Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91267353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCUS
FINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. SAMORE
                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
```

셤 οχ

```
mRNA EST 29-0CT-1996
mouse embryo 8 5dpc 10664019 Mus musculus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 258)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps 1;
                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
High quality sequence stops: 86
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                        Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.36e-02;
0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative full length read vector to vector length is 259 Seg primer: -28Ml3 revl from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"/clone="305291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 TTTTAATTTTTTGAAGTAAAGTTTT 203
                                                                                                               The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 tttgattttttacagtaaactttt 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 mo55b01.rl Life Tech mclone 557449 5'.
```

ô

Gaps

ö

US-08-713-928A-5.rsta

source

FEATURES

mRNA BASE COUNT

```
Numan clone=126573 library=Soares fetal liver spleen lNFLS vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=SP6 Resitel=Perc I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTATATTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                            ROG872 356 bp mRNA EST 03-APR-1995
yf11f11.s1 Homo sapiens cDNA clone 126573 3' similar to contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High qality sequence stops: 347
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                         226 aaaatatttttaaaattttaaaattttaatttnaatttnaaatttcaaataantttaaatta
                                                                                                                                                        288 CTTTTTTCATTTTATATTTTGAATGGAGTATTATCTTTTACAATAATATATCTTTTT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.36e-02;
0; Mismatches 24; Indels
                         Length 290;
                                                                          21; Indels
                         Score 26; DB 4; L
Pred. No. 3.36e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14;
                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/clone="126573"
/ 72 c 57 g 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson, R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                           Alu repetitive element; . R06872
                       5.6%;
Similarity 67.7%;
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.6%;
Best Local Similarity 66.7%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 TITITAATITI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 tctttattttt 88
                    Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g757492
EST.
                                                                                                                                                                                                                           286 taaat 290
                                                                                                                                                                                                                                                                          120 CAAAT 124
                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                            LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
S
                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 290)
Hillier,L., Clark, M., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soaree,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human clone-66694 library-Soares fetal liver spleen INFLS vector-pT7T3D (Pharmacia) with a modified polylinker host-bH10B (amplcillin resistant) primer-T7 RS1tel-Peo I RSite2-Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTATTATTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                         /organism="Mus musculus"
/strain="C57BL/6J"
/strain="C57BL/6J"
/note="Vector: pCWV-SPORT2; Site_1: Sall; Site_2: Not1;
Cloned unidirectionally. Primer: Oligo dT. 8.5dpc
embryos. pCMV-SPORT2 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the TWAGE-COMSOFFIEM (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 TATATAAAACTTTACTTCAAAAATTAAAAAAAAAAGAAGTATATTGTAAAAGATA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                          /clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
/dev_stage="8.5dpc embryos"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                            DB 145; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ../«/y 290 bp mRNA EST
ya53g12.r4 Homo sapiens cDNA clone 66694 5'.
T67279
g676719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
Other ESTs: ya53g12.s2.exp
Contact: Wilson Ry
WashU-Merck EST Project
WashIngton University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 145;
Pred. No. 3.36e-02;
                                                                                                                                                                                                                                                                                                 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
High qality sequence stops: 243
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                              30 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 g
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="66694
39 c
                                                                                                                                                                                                                                                                                                                                                                            5.6%;
                                                                                                                                                                                                                                                                                                    21
C
                                                                                                                                                                                                                                                                                                                                                                                                                             58; Conservative
                                                                                                                                                                                                                                                                          <1..>258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 58; Conser<sup>1</sup>
                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R.
```

11

RESULT

g ö DEFINITION

ACCESSION KEYWORDS ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

ö

Gaps

ö

source

FEATURES

BASE COUNT ORIGIN

DEFINITION

RESULT

ACCESSION NID. KEYWORDS ORGANISM

REFERENCE AUTHORS TITLE

COMMENT

```
1 (bases 1 to 375)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 371)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Kucaba, T., E., M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tan, F., Tanessis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA184881 375 bp mRNA EST 07-JAN-1997
mu46a04.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
642414 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 264
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 ITTACAATAATATACTTTCTTTTTTTTTTTTTTTTTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 51; Length Pred. No. 3.36e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 ttaataataattaacttttttatttatttattttttgagatggagtttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-Merck EST Project
Washington University School of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="187539
83 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.0%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91768527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheilenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                   AA034637 361 bp mRNA EST 21-JAN-1997
mh17a06.rl Soares mouse placenta 4NbMp13.5 14.5 Mus musculus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K05527 371 bp MRNA EST 04-AUG-1995
YP15h02.r1 Homo sapiens cDNA clone 187539 5' similar to contains
R83527
9928404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                       Vertebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
                                                                                                                                                          Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26; DB 188; Length 361; Pred. No. 3.36e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington.dhabversity School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector to vector length is 443
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="unknown"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.1%;
Matches 37; Conservative
                                                                                                                                                                                                                                                 to 361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e c
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                         clone 442738 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..361
                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                   91506498
```

source

FEATURES

mRNA BASE COUNT ORIGIN

14

RESULT

셤 ò LOCUS DEFINITION

ACCESSION NID

ö

Gaps

```
Score 26; DB 176; Length 375;
Pred. No. 3.36e-02;
0; Mismatches 11; Indels
                                                                                                                        98 t
                                                                                                                        689
                                                                                                                                  5.68;
"Best.Local Similarity....73.18;
Matches 37; Conservative
                                                                                                                        ದ
                                                                                                                 mRNA
BASE COUNT
ORIGIN
                                                   source
                                              FEATURES
```

Search completed: Tue Feb 3 20:05:54 1998 Job time : 968 secs.

g ò

ö

Gaps

***********	(AT)	Research Unit. of Edinburgh, U.K. tics, Inc.	ى بر	willion cell updates/sec					ann1 6:unann2 7:unann3 nann7 12:unann8 16:unann12 17:unenc	cale 0.667	by chance to have a he result being printed, distribution.		ion Pred. No.	mite allergen mag 29 1.73e+01 SPR28 protein - yeas 1.73e+01 dynamin-like protein 1.73e+01 dynamin-like protein 1.73e+01 dynamin-like protein 1.73e+01 testicular dynamin - 1.73e+01 dynamin, internal fo 1.73e+01 dynamin, internal fo 1.73e+01 dynamin - I fruit fi 1.73e+01 dynamin - I fruit fi 1.73e+01 hypothetical protein 2.57e+01 hypothetical protein 2.57e+01 heat shock protein 2.57e+01 dynamin II - human 2.57e+01 dynamin II - human 2.57e+01 dynamin II isoform a 2.57e+01 dynamin II isoform a 2.57e+01 dynamin II isoform a 2.57e+01
*****		. Collins, Biocomputing Rese 1994, 1995 University of E n rights by IntelliGenetics,	search, usir	1990, Maskai 81.629	-928A-10 USO8713928A.pep 8		80 residues	summaries	4:ann4 5:un unann6 11:u 15:unann11	Variance 32.486; sc	results predicted by to the score of the of the total score d	SUMMARIES	Description	559425 559425 559425 559425 67000000000000000000000000000000000000
**********	'' '-' 	2.1D John F. Coll t (c) 1993, 1994, Distribution righ	protein database	ated.	S-08-713-928A-10-8) from US08713 DYKDDDDK 8	0	segs, 30469580	Match 0% first 45	:53 :ann1 2:ann2 3:ann3 %*enemn4 9:unann5 10: 3:unann9 14:unann10 8:unrev	21.667; Vari	number of n or equal analysis	S	Length DB ID	45 9 00 00 00 00 00 00 00 00 00 00 00 00 0
*******		Release 2.1D Copyright (c) Distr	protein - pro	not	>0 (1 e: 56	le: PAM 150 Gap 15	95051	sing: Minimum Listing	pir53 1:an 1:an 1:an 1:an 13:u	Mean 2	No. is the greater the derived by	d	Query Match	4 4 4 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
****		, % ,	MPsrch_pp	Tabular output	Title: Description: Perfect Scor Sequence:	Scoring table	Searched:	Post-processing	Database:	Statistics:	Pred. score and is		Result No. Score	12 4 4 8 6 6 8 6 6 1 6 1 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1

	82.1 289 13 S16726 methylviologen-reduc 3.80e+01 306 13 S32834 methylviologen-reduc 3.80e+01 80.4 201 9 F40482 hypothetical protein 5.59e+01 80.4 201 9 F40482 hypothetical protein 5.59e+01 80.4 406 14 \$59296 probable finger prot 5.59e+01 80.4 408 13 \$45124 hypothetical protein 5.59e+01 80.4 483 13 \$45124 hypothetical protein 5.59e+01 80.4 483 13 \$45124 hypothetical protein 5.59e+01 80.4 408 1 PFRTGA platelet-derived gro 5.59e+01 80.4 1088 1 PFRTGA platelet-derived gro 5.59e+01 80.4 1089 1 PFRTGA platelet-derived gro 5.59e+01 80.8 10.8 10.8 10.8 10.8 10.8 10.8 10	#type c gen mag gen mag gen mag phagoide me Derma 5 #seque 2125 ujikawa, Y.; Oka Y.; Oka (1994) e dust e dust	protein 70 family. JX0313 LYDE MRNA 1-145 ##label AKI PC2125 LYDE protein ferences DDBJ:D17676 the nucleotide sequence for this amino acid inconsistent with that for D17676 in have additional nucleotide A at the code for mag29 #superfamily heat shock protein 70 ATP; heat shock; stress-induced protein #length 145 #molecular-weight 15594 #checksum	11arity 71.4%; Score 48; DB 8; Length 145; Conservative 2; Mismatches 0; Indels 0; Gaps 0; k 20
46 45 45 45 45 45 45 44 44 44 44 44 44 44	ᲓᲓᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡᲡ		രൂഡ് രൂഡ്ര	datch ss ryke ll: YKI

ô

Gaps

ö

/#authors

GÉNETICS #dene

ACCESSIONS

```
#authors Nakata, T.; Takemura, R.; Hirokawa, N.
#journal J. Cell Sci. (1993) 105:1-5
#title A novel member of the dynamin family of GTP-binding proteins is expressed specifically in the testis.
#cross-references MUID:93366923
                        #title Dynamin-like protein encoded by the Drosophila shibire gene associated with vesicular traffic. #cross-references WUID:91238973
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 #type complete dynamin-like protein - fruit fly (Drosophila melanogaster) #formal_name Drosophila melanogaster 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155498 #type complete
testicular dynamin - rat
#formal_name Rattus norvegicus #common_name Norway rat
25-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996
                                                                                                                                                                                                    nne shibire
##cross-references FlyBase:FBgn0003392
:Y #length 836 #molecular-weight 93671 #checksum 9040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         une FlyBase:shi
##cross-references FlyBase:FBgn0003392
XX #length 836 #molecular-weight 93730 #checksum 9048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #residues 1-848 ##label RES 1-848 ##cross-references GB:D14076; NID:g391871; CDS_PID:g391872 #cross-references GB:molecular-weight 95595 #checksum 9171
                                                                                                        preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##scatus preliminary; translated from GB/EMBL/DDBJ##molecule_type mRNA ##residues 1-840 ##1.
                                                                                                                                                                                                                                                                                 Score 48; DB 15; Length 836,
Pred. No. 1.73e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 15; Length 836 Pred. No. 1.73e+01; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van der Bliek, A.M.
submitted to the EMBL Data Library, May 1991
S17974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%; Score 48; DB 16;
            Nature (1991) 351:411-414
                                                                                                                                        1-836 ##label NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-836 ##label VAN
                                                                                                                                                                ##cross-references EMBL:X59435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:X59435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary
                                                                                                                                                                                                                                                                                 y Match 85.7%;
Local Similarity 71.4%;
hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 85.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                          ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
                                                                                      S15413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S17974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I55498
                                                                                                                                                                                                                                                                                                                                                           547 ykdedek 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547 ykdedek 553
                                                                                                                                                                                                                                                                                                                                                                                 |||:|:|
2 YKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:|:|
2 YKDDDDK 8
                                                                                                                                              ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
                                                                                                          ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status
                                                                                    #accession
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
            #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSIONS
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
ENTRY
TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                          #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #gene
                                                                                                                                                                                                                                            SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE
                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
S15413 #type complete
dynamin-like protein - fruit fly (Drosophila sp.)
#formal_name Drosophila sp.
21-Nov.1993 #sequence_revision 03-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dynamin 3 - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen, M.S.; Obar, R.A.; Schroeder, C.C.; Austin, T.W.; Poolry, C.A.; Wadsworth, S.C.; Vallee, R.B. Nature (1991) 351:583-588 Multiple forms of dynamin are encoded by shibire, a Drosophila gene involved in endocytosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #region nucleotide-binding motif A (P-loop)\
#region nucleotide-binding motif B\
#region nucleotide binding #status predicted
#length 836 #molecular-weight 93758 #checksum 9216
                                                                                                                                                                                                                                                                                                               #length 423 #molecular-weight 48193 #checksum 7812
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references FlyBase:FBgn0003392
DS alternative splicing; microtubule binding; P-loop
                                                                                                                  Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
S59425
                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 14; Length 423;
Pred. No. 1.73e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 15; Length 836;
Pred. No. 1.73e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S15413
S15413
van der Bliek, A.M.; Meyerowitz, E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #type complete
                                                                                                                                                                        ##molecule_type DNA
##residues 1-423 ##label MUR
##cross-references EMBL:248612
##experimental_source strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-836 ##label CHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references EMBL:X59448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #cross-references MUID:91260878
                                                                                                                                                                                                                                                                                                                                                   85.7%;
larity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-Feb-1997
S34399; S15497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity tches 7; Conse
                                                                              S59425
                                                                                                    S59423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S16130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534399
                                                                                                                                                                                                                                                                                                                                                                                                                               62 dydddddk 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 ykdedek 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [11:1:]
2 YKDDDDK 8
                                                                                                                                                                                                                                                                                             #map_position 4R
SUMMARY #le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues
  ALTERNATE_NAMES
ORGANISM
                                                                                                                                      #submission
                                                                                                                                                          . *accession
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #accession
```

m

RESULT ENTRY

TITLE ORGANISM

DATE

#authors #journal

#title

ACCESSIONS

REFERENCE

127-132 200-203

SUMMARY

RE -40

GENETICS #gene #authors

ACCESSIONS

REFERENCE

TITLE Organish

RESULT ENTRY

셤 ö DATE

ö

Gaps

ö

Gaps

ö

REFERENCE #authors

SUMMARY

ACCESSIONS

TITLE ORGANISM DATE

RESULT ENTRY

ð

```
ERENCE S15413

authors van der Bliek, A.W.; Meyerowitz, E.M.

#journal Nature (1991) 351:411-414

#title Dynamin-like protein encoded by the Drosophila shibire gene associated with vesicular traffic.

#cross-references MUD:91238973

#accession S17975
                                       A40671
van der Bliek, A.M.; Redelmeier, T.E.; Damke, H.; Tisdale,
E.J.; Meyerowitz, E.M.; Schmid, S.L.
J. Cell Biol. (1993) 122:553-563
Mutations in human dynamin block an intermediate stage in
coated vesicle formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dynamin-like protein - fruit fly (Drosophila sp.) #formal_name Drosophila sp. 22.Nov-1993 #sequence_revision 26-May-1995 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S16130 #type complete
dynamin 4 - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Chen, M.S.; Obar, R.A.; Schroeder, C.C.; Austin, T.W.; Poodry, C.A.; Wadsworth, S.C.; Vallee, R.B.
#journal Nature (1991) 351:583-586
#title Multiple forms of dynamin are encoded by shibire, a Drosophila gene involved in endocytosis.
#cross-references MUD:91260878
#accession S16130
                                                                                                                                                                                                                                                                       alternative splicing; GTP binding #length 864 #molecular-weight 97261 #checksum 8496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #length 883 #molecular-weight 98508 #checksum 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                        DB 15; Length 864;
                                                                                                                                                                                                                                                                                                                                      Score 48; DB 15; Le
Pred. No. 1.73e+01;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 15; Le
Pred. No. 1.73e+01;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references FlyBase:FBgn0003392
trons 834/3
                                                                                                                                                                                                                               ##residues 1-864 ##label VAN ##cross-references GB:L07807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1-883 ##label BLI
##cross-references EMBL:X59435
                                                                                                                                                                                        preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%;
larity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                   85.7%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S16130; S15498
S16130
    03-May-1994
A40671
                                                                                                                                                                                                            ##molecule_type mRNA
##residues 1-864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shibire
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                     A40671
                                                                                                                                                                                                                                                                                                                                                                                                                      553 ykddeek 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 ykdedek 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 YKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 YKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status
                                                                                                                                                                                             ##status
                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                 #authors
                                                                                                          #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #introns
                       ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSIONS
                                                                                                                              #title
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                         KEYWORDS
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
ORGANISM
DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
ORGANISM
DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                         #authors Ober, R.A.; Collins, C.A.; Hammarback, J.A.; Shpetner, H.S.; Vallee, R.B.

#journal Nature (1990) 347:256-261

itle Molecular cloning of the microtubule-associated mechanochemical enzyme dynamin reveals homology with a new family of GTP-binding proteins.

#cross-references MuID:90384564

#accession S11508
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A40671
van der Bliek, A.M.; Redelmeier, T.E.; Damke, H.; Tisdale, E.J.; Meyerowitz, E.M.; Schmid, S.L.
J. Cell Biol. (1993) 122:553-563
Mutations in human dynamin block an intermediate stage in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B40671 #type complete dynamin, internal form 2, short C-terminal form - human #formal_name Homo sapiens #common_name man 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                     D100 protein - rat Frat Fermina Frat Formion_name Norway rat #formal_name Rattus norvegicus #common_name Norway rat 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A40671 #type complete dynaminal form - human dynamin internal form 1 long C-terminal form - human #formal_name Homo sapiens #common_name man 03-May-1994 #sequence_revision 03-May-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
##residues_1-851 ##label OBA
##cross-references EMEL:X34531
##cross-references EMEL:X34531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alternative splicing; GTP binding
#length 851 #molecular-weight 96039 #checksum 7509
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 16; Length 851;
Pred. No. 1.73e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 15; Length 851;
Pred. No. 1.73e+01;
2; Mismatches 0; Indels
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
Pred. No. 1.73e+01;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coated vesicle formation
                                                                                                                                                                                        #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-851 ##label VAN ##cross-references GB:L07807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
##residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Query Match 85.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B40671
                                                          549 ykddeek 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 ykddeek 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    553 ykddeek 559
                                                                                                 2 YKDDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YKDDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YKDDDDK 8
```

α

RESULT

ద

å

ENTRY TITLE ORGANISM DATE

ö

Gaps

ö

#accession

KEYWORDS SUMMARY

qq

ORGANISM, DATE RESULT ENTRY

REFERENCE #authors

ACCESSIONS

ournal

itle

Length 883;

```
#accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                           TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
DATE
                                                                                        GENETICS
                                                                                                                                       SUMMARY
                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                          cerevisiae)
hypothetical protein YM9582.01c; hypothetical protein YM9581.01c; hypothetical protein YM9582.01c; hypothetical protein YM9582.01c; hypothetical protein 8 formal_name Saccharomyces cerevisiae 08-Jul-1995 #sequence_revision 09-Mar-1996 #text_change 23-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein N1665
#formal_name Saccharomyces cerevisiae
27-Apr-1996 #sequence_revision 03-May-1996 #text_change
23-May-1997
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Obermaier, B.; Piravandi, E.; Rinke, M.; Domdey, H. submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #length 1277 #molecular-weight 147040 #checksum 8885
                                                                                                                                    #region nucleotide-binding motif A (P-loop)\
#region nucleotide-binding motif B\
#region nucleotide binding #stetus predicted
#length 883 #molecular-weight 98536 #checksum 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S63130  #type complete
hypothetical protein YNL175c - yeast (Saccharomyces
cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                            S54451 #type complete
hypothotical protein YMR076c - yeast (Saccharomyces
                                                                               ##cross-references FlyBase:FBgn0003392
RDS alternative splicing; microtubule binding; P-loop
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 1277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, April 1995
S52836
                                                                                                                                                                                                                       Length 883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gentles, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
S54451
                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                     Score 48; DB 15; I
Pred. No. 1.73e+01;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 13; Pred. No. 1.73e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   659-1277 ##label PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##experimental_source strain AB972
NCE S52814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #experimental_source strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues 1-682 ##label GEN
. ##molecule_type mRNA
##residues 1-883 ##label v
##cross-references EMBL:X59449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references EMBL:249259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references EMBL:248952
                                                                                                                                                                                                                    ©Query Match 85.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.7%;
Best Local Similarity 85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             554451; 552836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
                                                                   shibire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 1265 dykdded 1271
                                                                                                                                                                                                                                                                                      547 ykdedek 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hap_position 13R
                                                                                                                                                                                                                                                                                                         |||:|:|
2 YKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||:|
1 DYKDDDD 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #submission
#accession
                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATE_NAMES ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors
#submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
#submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #accession
                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                  FEATURE
33-40
127-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                            KEYWORDS
                                                                     #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICS
                                                  GENETICS
                                                                                                                                                                                 SUMMARY
                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTRY
TITLE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mason, P.J.; Shiels, B.R.; Tait, A.; Beck, P.; Hall, R. Mol. Biochem. Parasitol. (1989) 37:27-36
Sequence and expression of a gene from Theileria annulata coding for a 70-kilodalton heat-shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A44985 #type complete
heat shock protein 70.1 - Theileria annulata
#formal_name Theileria annulata
28-ppr.1993 #sequence_revision 28-Apr-1993 #text_change
28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                               heat shock protein - yeast (Hansenula polymorpha)
#formal_name Hansenula polymorpha
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                 #Superfamily ribonucleoprotein repeat homology #length 403 #molecular-weight 45667 #checksum 9240
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diesel, A.A.; Roggenkamp, R.R. submitted to the EMBL Data Library, January 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #length 645 #molecular-weight 70137 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #length 646 #molecular-weight 70991 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSP70 genes of the yeast Hansenula polymorpha S41372
                                                                                                                                                                                          Score 47; DB 14; Length 403 Pred. No. 2.57e+01; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 83.9%; Score 47; DB 8; Length 646; Best Local Similarity 57.1%; Pred. No. 2.57e+01; Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 8; Len
Pred. No. 2.57e+01;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #superfamily heat shock protein 70 ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                           #type complete
                                   ##residues 1-645 ##label DIE ##cross-references EMBL: Z29379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-646 ##label MAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references GB:J04653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                        83.9%;
Similarity 50.0%;
4; Conservative
                     ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
##residues 1-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues 1-6
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
S63130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A44985
                                                                                                                                                                                                                                                                    79 eykedaek 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525 ykeedek 531
                                                                                                                                                                                                                                                                                            :||:| :|
1 DYKDDDDK 8
                                                                                                                 #map_position 14L
CLASSIFICATION #sup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||::|:|
2 YKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION
KEYWORDS
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #description
#accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
```

526 ykeedek 532 ||::|:| 2 YKDDDDK 8

Oy Oy

Search completed: Tue Feb 3 15:32:39 1998 Job time : 20 secs.

mailinger, eine me Erichenen

****	(TM)	*****
***	·	****
*		****
****		*******
***		*******
***		********

*	 	******
K K K K K		*****
k K K	r	* * *

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 3 15:31:48 1998; MasPar time 2.04 Seconds 83.171 Million cell updates/sec rabular output not generated.

>US-08-713-928A-10 (1-8) from US08713928A.pep 56 Description: Perfect Score: Title:

1 рукророж 8 Sequence:

PAM 150 Gap 15 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot34 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11

Mean 22.506; Variance 27.580; scale 0.816

Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No.	1.53e+00	1.53e+00	1.53e+00	1.53e+00	1.53e+00	1.53e+00	1.53e+00	7.21e+00	7.21e+00	7.21e+00	7.21e+00	7.21e+00	7.21e+00	7.21e+00	1.14e+01	1.14e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	101101
Description	ALLERGEN MAG29 (FRAGM	DYNAMIN 3 (DYNAMIN, T	OYNAMIN-1 (D100) (DYN 4	OYNAMIN-1 (DYNAMIN BR 4	VYNAMIN-1.	OYNAMIN.	OYNAMIN (SHIBIRE PROT	HYPOTHETICAL 45.7 KD	HEAT SHOCK PROTEIN 70	HEAT-SHOCK PROTEIN 70	HEAT SHOCK 70 KD PROT	OYNAMIN 2 (DYNAMIN UD	DYNAMIN 2.	DYNAMIN 2.	PROBABLE E4 PROTEIN.	PROBABLE E4 PROTEIN.	HYPOTHETICAL 23.6 KD	SNP1 PROTEIN.	ALPHA PLATELET-DERIVE	ALPHA PLATELET-DERIVE	ALPHA PLATELET-DERIVE	, wremone representative
e e	MA29_DERFA #	DYN3_RAT I	ч	三 三 三	DYN1_HUMAN I	DYN1_CAEEL I	DYN_DROME I	-		_		DYN2_MOUSE I	_	_	VE4_HPV04 I	_	Y007_NPVAC	ENP1_YEAST I	PGDS_RAT 1	PGDS_HUMAN 2	PGDS_MOUSE 1	
DB	9	m	m	٣	٣	m	ო	11	Ŋ	Ŋ	Ŋ	ო	٣	က	10	10	10	ო	7	7	^	
Length	145	848	851	861	864	865	883	403	642	644	646	866	870	870	181	213	201	account 8-3.	1088	1089	1089	
Query Match	85.7	85.7	85.7	85.7	85.7	85.7	85.7	83.9	83.9	83.9	83.9	83.9	83.9	83.9	82.1	82.1	80.4	man B. Ost, 400	80.4	80.4	80.4	200
Score	48	48	48	48	48	48	48	47	47	47	47	47	47	1 47	46	46	45	min A.Sm	45	45	45	7
	r-1	~1	m	7	ហ	9	7	œ	6	21	11	12	13	.14	12	16	17		13	20	21	ç

2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	۲.	2.79e+01	2.79e+01	2.79e+01	2.79e+01	4.31e+01	4.31e+01	4.31e+01	4.31e+01	4.31e+01	6.61e+01	6.61e+01	6.61e+01	6.61e+01	•	6.61e+01	6.61e+01
COAT PROTEIN.	COAT PROTEIN.	COAT PROTEIN.	COAT PROTEIN.	COAT PROTEIN.	VARIANT SURFACE GLYCO	HEAT SHOCK PROTEIN 70	HEAT SHOCK PROTEIN 70	CELL SURFACE PROTEIN	PROBABLE TREHALASE (E	DNA POLYMERASE (EC 2.	HYPOTHETICAL PROTEIN	REGULATORY PROTEIN E2	CAPSID PROTEIN P40 (C	CARBON MONOXIDE DEHYD	BNI1 PROTEIN (SYNTHET	HYPOTHETICAL 23.7 KD	_	HYPOTHETICAL 54.6 KD	HYPOTHETICAL 68.8 KD		HYPOTHETICAL 167.1 KD	HYPOTHETICAL 287.5 KD
COAT_CAMVC	COAT_CAMVE	COAT_CAMVN	2 COAT_CAMVS C	COAT_CAMVD	VSI4_TRYBB	HS71_ANOAL	HS72_ANOAL	_	TREB_YEAST	DPOM_MAIZE	Y051_HAEIN		VP40_HSV7J	_	BNI1_YEAST	YAB4_YEAST	YDBI_SCHPO	YGZ4_YEAST	11 YAG7_YEAST H	YJB9_YEAST	YGU7_YEAST	YBA4_YEAST
488		488		490	514 3	640	640	762	780	929			512 1					458			_	2493
78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	76.8	76.8	76.8	76.8	76.8	75.0	75.0	75.0	75.0	75.0	75.0	75.0
44	44	44	44	44	44	44	44	44	44	44	43	43	43	43	43	43	42	42	42	42	42	42
23	24	22	56	27	78	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ő

Pred. No. 4.53e+00;

N

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
               Gaps
                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S11508; S11508.
PROSITE: PS00410; DYNAMIN.
PROSITE; PS50003; PH_DOMAIN.
MOTOR POTEIN; GTP-BINDING; MICROTUBULES; MULTIGENE FAMILY;
ENDOCYTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLINE; 90384564.
OBAR R.A., COLLINS C.A., HAMMARBACK J.A., SHPETNER H.S.,
VALLEE R.B.;
NATURE 347:256-261(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 3; Leng
Pred. No. 4.53e+00;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                       GTP (BY SIMILARITY)
GTP (BY SIMILARITY)
GTP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                               033F72CA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO-RICH.
6D4974F6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP (POTENTIAL).
GTP (POTENTIAL).
GTP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DYNAMIL 1 (D100) (DYNAMIN, BRAIN) (B-DYNAMIN)
DNHI OR DNM.
RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                              621 F
95595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%;
illarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 851
95927 }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X54531; G56054; -.
                                                                                                                                                                                                                                                                                                                         45
140
208
                                                                                                                                                                                                                                                                                                                                       136
205
215
515
648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38
136
205
519
753
851 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
 MEDLINE; 93366923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 ykddeek 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 УКООООК 8
                                                                                                                                                                                                                                                                                                    ENDOCYTOSIS
                                                                                                                                                                                                                                                                                                                   NP_BIND
NP_BIND
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JT 3
DYN1_RAT
P21575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
NP_BIND
NP_BIND
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE KEEP BOOK OF COCCOCCE FOR THE FEET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

DB 3; Length 851;

Score 48;

85.7%;

Query Match

```
ı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                 ö
                                                                                                                                                                                                                                                                                                                              STEEF A., DER PUTTEN H.;
STRAIM-NIH SWISS;
STIEF A., DER PUTTEN H.;
SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN INVOLVED
-!- FUNCTION: MICROTUBULE BUNDLES AND ABLE TO BIND AND HYDROLYZE
GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN
PARTICULAR ENDOCYTOSIS.
-!- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED.
-!- SUBCELLULAR COLATION: MICROTUBULE-ASSOCIATED.
-!- SIMILARITY: CONTAINS A PH DOMAIN.
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 93328758.
VAN DER BLIEK A.M., REDELMEIER T.E., TISDALE E.J., MEYEROWITZ E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNMI OR DNM.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95153276.
DOWNING A.K., DRISCOLL P.C., GOUT I., SALIM K., ZVELEBIL M.J.,
WATERFIELD M.D.;
                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L31397; G487857; -.
PROSITE: PS00410; DYNAMIN.
PROSITE: PS50003: PLNOMAIN.
MOTOR PROTEIN; GTP-BINDING; MICROTUBULES; MULTIGENE FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 3; Length 861;
Pred. No. 4.53e+00;
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   864 AA.
                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL BIOL. 122:553-563(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF 511-630
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REL. 28, 0
(REL. 28, 1
(REL. 34, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                               553 ykddeek 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 ykddeek 555
                                                                            æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                 ||||::|
2 YKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 YKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHMID S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5

1D DYLL HUMAN

AC 00513;
DT 01-FEB-1994

DT 01-FEB-1994

DT 01-CT-1996

DE DYNAMIN 1.

GN DWM OR DWM.

OC EUKARYOTA; M

OC EUTARRYOTA; M

OC EUTARRYOTA; M

OC EUTARRYOTA; M

CEMBOLINE; 93;
RA VAN DER BLIF

RA VAN DER BLIF

RA SCHMID S.L.;

RA DOWNING A.K.

RA DOWNING A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

```
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
268
594
883 AA;
                                                                                                                                                                                                                       STRAIN-CANTON-S;
MEDLINE; 91260878.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 ykdedek 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENDOCYTOSIS
     JT 7
DYN_DROME
P27619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
       RESULT
                                           g
CURR. BIOL. 4:884-891(1994).

C. !- FUNCTION: MICROTUBLELE-ASSOCIATED FORCE-PRODUCING PROTEIN INVOLVED IN PRODUCING MICROTUBLELE-ASSOCIATED FORCE-PRODUCING PROCESSES.

IN PRODUCING MICROTUBLE SUDDLES AND ABLE TO BIND AND HYDROLYZE GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN PARTICULAR BINDOCYTOSIS.

C. !- SUMILARITY: BELONGS TO THE DYNAMIN FAMILY.

C. !- SIMILARITY: CONTAINS A PH DOMAIN.

EMBL: LO7809; G181849; -...

EMBL: LO7809; G181855; ALT_SEQ.

REMBL: LO7809; G181855; ALT_SEQ.

REMBL: LO7810; G181855; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                               MOTOR PROTEIN, GTP-BINDING; MICROTUBULES; MULTIGENE FAMILY; ENDOCYTOSIS.

NP_BIND 38 45 GTP (BY SIMILARITY).

NP_BIND 136 140 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L29031; G456286; -.
PROSITE; PS00410; DYNAMIN.
PROSITE; PS50003; PH_DOMAIN.
MOTOR PROTEIN; GTP-BINDING; MICROTUBULES; MULTIGENE FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 3; Length 865;
Pred. No. 4.53e+00;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 3; Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.53e+00;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D916F54 CRC32;
                                                                                                                                                                                                                                                                                                                                                                  97E7D339 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                          45 GT
140 GT
208 GT
625 PH
97407 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91-TEB-1995 (REL: 31; CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   85.7%;
similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 85.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                          38
136 1
205 2
519 6
864 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
207
519
65 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553 ykddeek 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552 ykddeek 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKDDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKDDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENDOCYTOSIS.
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
LD...aDVN1_CAEEL
AC P39055;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYNAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREAC OOS OF THE COLOR OF THE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
ö
                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN WHICH IS INVOIVED IN THE PRODUCTION OF MICROTUBULE BUNDLES AND WHICH IS ABLE TO BIND AND HYDROLYZE GTP. SHIBIRE IS IMPLICATED IN ENDOCYTIC PROTEIN SORTING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: SHIBIRE MUTATION IS THE CAUSE OF TEMPERATURE-SENSITIVE PRRALISSIS. THIS IS BELIEVED TO BE DUE TO A REVERSIBLE BLOCK OF ENDOCYTOSIS, WHICH PREVENTS MEMBRANE CYCLING AND THUS DEPLETES SYNAPTIC VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOTOR PROTEIN; GTP-BINDING; MICROTUBULES; ALTERNATIVE SPLICING;
                                                                                                                                                                                                 CHEN M.S., OBAR R.A., SCHROEDER C.C., AUSTIN T.W., POODRY C.A. WADSWORTH S.C., VALLEE R.B.;
NATURE 351:583-586(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN THIRD FORM).
V -> R (IN SHORT FORM).
MISSING (IN SHORT FORM).
G -> S (IN SHI-TS2 MUTANT).
G -> D (IN SHI-TS1 MUTANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                      EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 3; Le
Pred. No. 4.53e+00;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> K.
489F2ED4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP (POTENTIAL).
GTP (POTENTIAL).
GTP (POTENTIAL).
                         01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-EBB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DYNAMIN (SHIBIRE PROTEIN).
883 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PH.
PRO-RICH.
                                                                                                                                                                                                                                                                               STRAIN=OREGON-R;
MEDLINE; 91238973.
VAN DER BLIEK A.M., MEYEROWITZ E.M.;
NATURE 351:411-414(1991).
                                                                                                       DROSOPHILA MELANOGASTER (FRUIT FLY).
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.7%;
larity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2007
621
833
833
883
141
141
594
98537 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 YKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
```

US-08-713-928A-10.rsp

```
01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-011-1993 (REL. 26, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN (HSP 70.1).
THEILERIA ANNULATA.
EUKARYOTA; PROTOZOA; APICOMPLEXA; SPOROZOA; COCCIDIA; PIROPLASMIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAPERONE; HEAT SHOCK; ATP-BINDING; MULTIGENE FAMILY; ACETYLATION INIT_MET 0 BY SIMILARITY.
MOD. RES 1 ACETYLATION (BY SIMILARITY).
SEQUENCE 644 AA; 70006 MW; D6C78F84 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DYNAMIN 2 (CHYMAIN UDINY).
DNM2 OR DYN2.
MUS MOSCULUS (MOUSE).
EUKARYCHA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
                                                                                                                                                                                                                    TITORENKO V.I., EVERS M.E., DIESEL A., SAMYN B., VAN BEEUMEN J ROGGENKAMP R.R., KIEL J.A.K.W., VAN DER KLEI I., VEENHUIS M.; YEAST 12:849-857(1996).
-!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
-!- FUNCTION: BY HEAT SHOCK.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; Z29379: G443915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 5; Length 644; Pred. No. 7.21e+00; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 5; Length 646; Pred. No. 7.21e+00; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASON P.J., SHIELS B.R., TAIT A., BECK P., HALL R.;
MOL. BIOCHEM. PARASITOL. 37:27-36(1989).
-1 - SHILLARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; J04663; 161869; -.
HSSP; P19120; INGG.
PROSITE; PS00297; HSP70_1.
PROSITE; PS003297; HSP70_2.
PROSITE; PS003297; HSP70_3.
ATP-BINDING; HEAT SHOCK.
                                                      HANSENULA POLYMORPHA (YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646 AA; 70973 MW; C2EB974B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               646 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      866 AA
                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-ATCC 34438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
HEAT-SHOCK PROTEIN 70 1 (HSP72)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.9%;
llarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 83.9%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 90136713.
                                                                                                                                                                         STRAIN=ATCC 34438;
MEDLINE; 96437974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 ykeedek 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 ykeedek 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||::|:|
2 YKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||::|:|
2 YKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 12
DYN2_MOUSE
P39054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS70_THEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P16019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OCCUPATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

CC -1- SUBLITED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

CC -1- SUBLIBATITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RNP).

CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RNP).

CC -1- SUBCELLULAR LOCATION: NUCLEAR PROTEIN: RNA-BINDING.

KW HYPOTHETICAL PROTEIN; NUCLEAR PROTEIN: RNA-BINDING (RNP2) (BY SIMILARITY).

FT DOMAIN 144 149 RNA-BINDING (RNP2) (BY SIMILARITY).

FT DOMAIN 241 246 RNA-BINDING (RNP2) (BY SIMILARITY).

NOMAIN 280 287 RNA-BINDING (RNP2) (BY SIMILARITY).

Ang Aa: 45667 MW; D3D18998 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                    01-00T-1996 (REL. 34, CREATED)
01-00T-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 45.7 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 11; Length 403;
Pred. No. 7.21e+00;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 5; Length 642;
Pred. No. 7.21e+00;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID HS72_PICAN STANDARD; PRT; 642 AA. AC P53623; P53422; P53422
                                                                                                                                                                                                                                                 SÄCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34, CREATED)
34, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
                                                      403 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       644 AA
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.9%;
Similarity 57.1%;
4; Conservative
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 eykedaek 86
                                                                                                                                                                                                                       YNL175C OR N1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522 ykeedek 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 YKDDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P53421;
01-OCT-1996 (
01-OCT-1996 (
01-OCT-1996 (
                                                YNR5_YEAST
P53883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 10
HS71_HANPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

→ Best Loc
→ Matches

                      RESOLT

TO SENT THE SOLT

TO SENT THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRCRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8484A
```

ö

Gaps

ö

ö

Gaps

ö

Gaps

ö

0; Indels

```
MEDLINE; 96011652.

MEGROTUGULE ASSOCIATED FORCE-PRODUCING PROTEIN INVOLVED IN PRODUCING MICROTUGULE BUNDLES AND ABLE TO BIND AND HYDROLYZE GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN PARTICULAR ENDOCYTOSIS.

MERCHALLIAN LOCATION: MICROTUBULE-ASSOCIATED.

MERCHALLIANI LOCATION: MICROTUBULE-ASSOCIATED.

MERCHALLIANI SELONGS TO THE DYNAMIN FAMILY.

MERCHALLIANI STP-BINDING; MICROTUBULES; MULTIGENE FAMILY;

ENDECYTOSIS; ALTERNATIVE SPLICING.
                                           GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

PH.

LAFBAIVKKQVVKLKEPCLKCVDLVIQELISTVRQCTS

MAFEAIVKKQLVKLKEPSLKCVDLVVSELATVIKKCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNM2 OR DYN2.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                          (IN FORM IIAA).

MISSING (IN FORM IIC).

S -> T (IN REF. 1).

S -> T (IN REF. 1).

N -> K (IN REF. 1).

MISSING (IN REF. 1).

GPTFCP -> PHTGA (IN REF. 1).

GPTFCP -> PHTGA (IN REF. 1).
MICROTUBULES; MULTIGENE FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 3; Length 870;
Pred. No. 7.21e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN A FORM)
16C963CA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 3; L
Pred. No. 7.21e+00;
3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 870 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                            ALTERNATIVE SPLICING
                                                                                                                                                                                                                    519 M.
298 S
389 S
487 N
637 G
719 MI
791 GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98018 MW;
  GTP-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                           83.9%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.18;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                45
140
208
625
444
                                                                                                                                                                                                                                                                                                                     637
719
786
870 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 ykdeeek 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553 ykdeeek 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||:::|
2 YKDDDDK 8
MOTOR PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 YKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYN2_HUMAN
P50570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
ID VE4_HPV04
AC Q07852;
                                                                       NP_BIND
NP_BIND
DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYNAMIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                       VARSPLIC
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
                                                NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT TO THE SULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                        C STRAIN-NIH SWISS;

A STEEF A., DER PUTTEN H.;

STRAIN-NIH SWISS;

C STRAIN-NIH SWISS;

STRAIN-NIH SWISS;

SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

- FONCTION: MICROTUBULE BUNDLES AND ABLE TO BIND AND HYDROLYZE GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN PARTICULAR ENDOCYTOSIS.

- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED.

- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.

- SIMILARITY: BELONGS TO THE DYNAMIN. FAMILY.

EMBL; 131388; 6487874; - -

R PROSITE; PSO0410; DYNAMIN.

R PROSITE; PSS0003; PH_DOMAIN.

M MOTOR PROFIEIN; GTP-BINDING; MICROTUBULES; MULTIGENE FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 94140890.

SONTAG J. M., FYKSE E.M., USHKARYOV Y., LIU J.-P., ROBINSON P.J.,
SUEDHOF T.C.;
J. BLOL. CHEM. 269:4547-4554(1994).

-!- FUNCTION: MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN INVOLVED
IN PRODUCING MICROTUBLE BUNDLES AND ABLE TO BIND AND HYDROLYZE
GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN
PARTICULAR ENDOCYTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED.
-1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED, INCLUDING THE BRAIN.
HIGHEST LEVELS IN THE TESTIS.
-1- ALTERNATIVE PRODUCTS: THREE FORMS OF DYNZ CAN BE PRODUCED BY
LY ALTERNATIVE SPLICING: THE FORM SHOWN (IIBA) DIFFERES FROM IIAA
BY THE REPLACEMENT OF AN EXON BY ANOTHER ONE WHICH IS HIGHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 3; Length 866;
Pred. No. 7.21e+00;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE DAWLEY;
MEDLINE; 94119943.
COOK T.A., URRUTIA R., MCNIVEN M.A.;
PROC. NATL. ACAD. SCI. U.S.A. 91:644-648(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5CB0DE3B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.
-!- SIMILARITY: CONTAINS A PH DOMAIN.
EMBL; L25605; G416396; -.
EMBL; L24562; G404073; -.
EMBLS; PS00410; DYNAMIN.
PROSITE; PS50003; PH_DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEE-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            870 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.9%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATTUS NORVEGICUS (RAT)
                         SEQUENCE EROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    38
136
205
515
866 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549 ykdeeek 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNM2 OR DYN2.
                                                                                                                                                                                                                                                                                                                                                                                        ENDOCYTOSIS.
NP_BIND
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 13
DYN2_RAT
P39052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYNAMIN 2
```

g

ŏ

ö

Gaps

ö

0; Indels

Length 870;

```
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DE PROBABLE E4 PROTEIL
OS HUMAN PAPILLOMAVIRUS TYPE 4.
OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.
RR. MEDLINE; 93276568.
RA MEDLINE; 93276568.
RA MEDLINE; PAPILIOS H., MATSUKURA T., KAWASHIMA M., DE VILLIERS E.M.;
CVIROLOGY 194789-799(1993).
DR EMBL; X70827; G312089; --
KW EARLY PROTEIN.
FT DOMAIN 133 142 POLY-GLU.
FT DOMAIN 133 20849 MW; 2769F837 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

82.1%; Score 46; DB 10; Length 181;
Best Local Similarity 62.5%; Pred. No. 1.14e+01;
Matches 5; Conservative 2; Mismatches 1; Indels
                        DT 01
DT 01
DT 01
DE PU
SO NH H
WANTER NAME OF THE NAME OF THE NAME OF THE OF T
```

112 dydeddek 119 || :||:| | DYKDDDDK 8

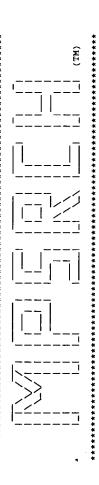
ö

Gaps

ö

Search completed: Tue Feb 3 15:32:01 1998 Job time: 13 secs.

5



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm Tue Feb 3 15:32:58 1998; MasPar time 2.41 Seconds 46.200 Million cell updates/sec MPsrch_pp

>US-08-713-928A-10 (1-8) from US08713928A.pep 56 Title: Description: Perfect Score:

Tabular output not generated.

1 DYKDDDDK 8 Sequence:

PAM 150 Gap 15 Scoring table:

111726 seqs, 13889129 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part13:part13 11:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 a-geneseq30

Variance 46.181; scale 0.329 Mean 15.190; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

)		æ					
Result No.	Score	Query Match	Length	DB	G.	Description	Pred. No.
1	56	100.0	. 80	23	W00971	FLAG epitope.	6.57e+00
7	26	100.0	80	22	W18236	FLAG epitope.	6.57e+00
m	56	100.0	80	15	R91066	Affinity tag peptide.	6.57e+00
4	56	100.0	۵	15	R87022	Flag octapeptide.	6.57e+00
S	26	100.0	æ	16	R91045	Antigenic N-terminal	6.57e+00
9	26	100.0	80	~	P70024	N-terminal fusion con	6.57e+00
7	56	100.0	œ	m	R09327	Sequence of N-termina	6.57e+00
80	56	100.0	13	23	W00969	FLAG epitope with nuc	6.57e+00
6	26	100.0	13	٣	P60023	Sequence of a Di-Palm	
10	26	100.0	27	σ	R46933	Hyperglycosylated hil	6.57e+00
11	26	100.0	28	П	P82355	Fusion protein for ex	
.12	26	100.0	75	23	W26361	Human pancreatic secr	6.57e+00
13	26	100.0	78	23	W26363	hPSTI.OMTKY3 chimeric	6.57e+00
14	26	100.0	78	23	W26364	hPSTI.SSImutant chime	6.57e+00
15	26	100.0	84	23	W00945	CMV500-4heptadCREB (N	6.57e+00
9	56	100.0	96	23	W26362	hPSTI.SSI chimeric su	6.57e+00
17	26	100.0	97	23	W00949	CMV500-4HeptadFos leu	6.57e+00
18	26	100.0	105	23	W00947	CMV500-Fosb2IP(MO) pr	6.57e+00
19	26	100.0		23	W00950	CMV400-JunbZip leucin	6.57e+00
20	26	100.0	122	16	R90842	Recombinant flag simi	6.57e+00

ö

Gaps

ö

Score 56; DB 23; Length 8; Pred. No. 6.57e+00; 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative

1 dykddddk 8 ||||||||| 1 DYKDDDDK 8

8 á

6.55 6.55 6.55 6.55 6.55 6.55 6.55 6.55
Human IL-3 mutant for Human IL-3 mutant for Glycophorin antibody Anti-influenza N10 sc Ly-2+Ly-3 V domain wi Sequence of psc49FLAG Flag tag/VT1 A subuni Flag tag/VT2 A subuni Aggrecanase artificia Aggrecanase alphanan glucocerebrosid (FRP5)-ETA fusion procev(FRP5)-ETA fusion procev(FRP5)-ETA fusion scrv(FRP5)-ETA fusion scrv(FRP5)-ETA fusion scrv2(FRP5)-FRP5)-ETA scrv2(FRP5/FRP5)-ETA scrv2(FRP5/FRP5)-ETA scrv2(FRP5/FRP5)-ETA
R78367 R78366 R52864 R52865 R38321 W06414 W18574 W18574 W05137 R26983 R26983 R26983 R2604 W05138 R2604 W05144 W05144
00000000000000000000000000000000000000
1125 1125 125 126 127 127 127 127 127 127 127 127 127 127
000000000000000000000000000000000000000
<i>Ე Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა</i>
22222222222222222222222222222222222222

ALIGNMENTS

ę.

```
09-NOV-1995; U05348.
28-APR-1994; US-235397.
(IMMV) IMMUREX CORP.
(UMOR) UNIV MISSOURI.
(USSH) US NAT INST OF HEALTH.
Alderson M, Armitage RJ, Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Peptide; 8 AA.
                                                                                                                standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hutt-fletcher LM,
WPI; 95-393086/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or viral infection.
                                                                                                                                                                                                    Flag octapeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DYKDDDDK 8
  DYKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 dykddddk 8
                                                                                                                                                                                                                                                                                                                                                                        inteleukin-7
                                                                                                                                       R87022;
11-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 5
R91045 S'
R91045;
                                                                                                          R87022
                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-1996.
11-SEP-1995; U12037.
10-SEP-1994; U230357.
(NEUR-) NEUROCKINE BIOSCIENCES INC.
Clevenger W, DeSouza EB, Liaw CW, Lovenberg TW;
Oltersdoof T T;
Interleukin-1 type 3 receptor proteins - useful for the treatment of immune-associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Totalm 6: Page 37; 111pp; English.

The FLAG epitope (W18236) is utilised in novel constructs for expression of lysosomal enzymes, e.g. human glucocerebrosidase and alpha-L-iduronidase in transgenic plants. The epitope coding sequence is fused in frame to the C-terminus of the lysosomal enzyme coding sequence (see also T71753) in order to facilitate the detection and purification of the gene product (see also W18237). It is designed to be a hydrophilic marker peptide situated on a protein surface to facilitate antibody interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                          20-MAR-1997.
13-SEP-1995; U14730.
14-SEP-1995; U16730.
14-SEP-1995; US-003737.
(CROP-) CROPTED BOY CORP.
(VIRG ) VIRGINIA TECH INTELLECTUAL PTY INC.
(Cramer CL., Oishi KK, Radin DN, Welssenborn DL;
WPI; 97-202248/IN Radin DN, Welssenborn DL;
Production of enzymatically active (modified) lysosomal enzyme in transgenic plants - useful in treatment of lysosomal storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Affinity tag peptide. Interleaving the second of the secon
                                                                                                                                                                                     Lysosomal enzyme; lysosome; transgenic plant; glucocerebrosidase; alpha.L.iduronidase; IUDA; enzyme replacement therapy; Gaucher disease; Hurler syndrome; FLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 7, 64pp; English.

An affinity tag (R91066) may be linked to interleukin-1 type-3 receptors (see e.g. R91064 and R91054) produced by recombinant DNA technology. The peptide facilitates purification of the expressed recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 22; Length 8; Pred. No. 6.57e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 15; Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50, Pred. No. 6.57e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                           .T 2
W18236 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ו
(91066 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%;
Matches 8: Control of Autches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-1996 (first entry)
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 dykddddk 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 dykddddk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9607739-A2.
                                                                                                                                                                                                                                                                                                         WO9710353-A1.
                                                                                                                                                              FLAG epitope.
                                                                                                       W18236;
01-OCT-1997
                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

Best Loc Matches

셤 å 윱

38888888888

```
Example 1: Page 38: 51pp: English.

Example 1: Page 38: 51pp: English.

This sequence represents the Flag octapeptide, and was used in creating a This sequence represents the Flag octapeptide, and was used in creating a Exist.

Example 1: Page 38: 51pp: English.

Example 1: Page 38: 51pp: English.

Example 20: Example 20: English.

Example 20: Example 20: English.

Example 20: Exist.

Example 20: English.

Example 
BZLF2; epstein-barr virus; EBV; C-type lectin; beta chain; MHC; antigen; major histocompatibility complex; immunoglobulin; cytotoxic T cell; autoimmune disease; myasthenia gravis; multiple sclerosis; allergy; systemic lupus erythematosus; organ transplant rejection; asthma; IL-7; tissue transplant rejection; therapy; cancer; viral disease; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AldG-1996 (first entry)
Antigenic N-terminal peptide for fusion to shull-1R.
Interleukin-1 receptor; human; soluble; N-terminal peptide; antigen; epitope; shull-1R; monoclonal antibody; bovine mucosal enterokinase; interleukin-1; IL-1; immune response; marman; diagnosis; therapy; regulation; immune disease; inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epstein-Barr virus BZLF2 fusion proteins - used for treating e.g. auto-immune disease, transplant rejection, allergy, asthma, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     age RJ, Cohen JI, Comeau MR, Farrah TM;
Spriggs MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 15; Length 8;
Pred. No. 6.57e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5492888-A.
20-FEB-1996.
25-NOV-1987; 125627.
25-NOV-1987; US-125627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
1D R9
AC R9
DT 01
DE AD
DE AD
KW 1D
KW 1E
KW 1E
KW 1E
COS S1
PP 22
PR 21
```

US-08-713-928A-10.rag

ន្តម្ភម្ជ

g ð

```
29-MAR-1992 (first entry)
Sequence of N-terminal octapeptide for compsn. contg. human
                                                                 interleukin-3 (IL-3) analogue.
Lymphokine, bone marrow proliferation; cytopenia therapy.
W09001039-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-1997.
31-7UL-1996; U12590.
31-JUL-1996; US-001654.
31-JUL-1995; US-001654.
29-MAY-1996; US-018496.
(KRYL/) KRYLOV DEPT HEALTH & HUMAN SERVICES.
(VINS/) VINSON C R.
                                                                                                                                                                                         Anderson DM, Cosman DJ, Price VL; WPI; 90-067162/09.
                                                                                                                                                                                                                                                                                 Claim 5; Page 18; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W00969 standard; Peptide; 13 AA.
R09327 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                      08-FEB-1990.
14-JUN-1989; U02599.
20-JUL-1988; US-221699.
(IMMU-) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vinson CR;
                                                                                                                                                                                                                                                              treating cytopenias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dykddddk 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DYKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
WO9705249-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krylov D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                   Disclosure; Column 8; 22pp; English.

This sequence represents an antigenic N-terminal peptide epitope. This sequence can be fused to soluble human interleukin-1 receptor (shuIL-IR) by using this sequence, recombinant shuIL-IR can be assayed and purified easily, by using a monoclonal antibody that reversibly binds this epitope. By using bovine mucosal enterokinase, this sequence can be elaved from the recombinant shuIL-IR. Proteins capped with this peptide may also be resistant to intracellular digestion in E. coli. The shuIL-IR can be used in a method for suppressing interleukin-1 (IL-1) administering an effective amount of shuIL-IR to the mammal, preferably in a dose of 500mg-5mg/kg/day. The shuIL-IR is effective for use in activities, in contrast to membrane-bound full-length mature IL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obtd. by recombinant DNA methods in high yields, used for potentiating immune responses, treating leukaemias etc.

Disclosure; Page 13; 37pp; English.

The sequence encodes a fusion contruct which links a mutant sequence of human granulocyte-colony stimulating factor to a yeast alpha-factor leader sequence. Fusion proteins capped with this peptide are resistant to intracellular degradation.

See also N70029, N70031-35 and P70025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                 WPI; 96-150236/15.
Use of sol. IL-1 receptors to suppress IL-1-mediated immune
responses - e.g. for treatment of inflammation in mammals, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1991 (first entry)
N-terminal fusion construct comprising mutant human G-CSF and yeast alpha-factor leader sequence.
Granulocyte-colony stimulating factor; fusion protein; yeast alpha-factor leader sequence.
EP-243153-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 16; Length 8;
Pred. No. 6.57e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 2; Length 8;
Pred. No. 6.57e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cosman DJ, Gillis S, Mochizuki DY, March CJ, Price VL,
Tushinski RJ, Ordal DL.
WPI; 87-300791/43.
                                                                   Dower SK, March CJ, Sims JE, Urdal DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P70024 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 100.0%;
Local Similarity 100.0%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
            21-DEC-1989; US-455488.
17-JUN-1992; US-904071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1987.
22-APR-1987; 303509.
22-APR-1986; US-856643.
14-NOV-1986; US-931458.
                                                 (IMMV ) IMMUNEX CORP.
                                                                              96-150236/15.
                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 dykddddk 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DYKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DYKDDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 dykddddk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNEX Corp.
                                                                                                                                                                                                                                                                                                                                                                                                          receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

RESULT ID P7 AC P7 DD 112 DD N-DD N-DD Y-EW Gr KW Y-EP PD 28

Ţ

셤

្ត្រីដូ<u>ឌ្</u>ឌីឌីឌីឌីឧប្តីប្រកួប

```
Claim 16; Page 54; 144pp; English.

This peptide sequence comprises a FLAG epitope with a nuclear localisation sequence. It is used in novel modified nucleic acid binding protein (NABPs) chimeras. These claimed NABPs, esp. leucine zipper proteins and bHLH proteins, have an appended acidic extension peptide (see W00958-65). They can regulate the function of a target nucleic acid or gene to which they are bound, and act as potent dominant-negative regulators of gene transcription, cell growth and cell proliferation. They can be used in cancer therapeutics, to treat diseases caused by eukaryotic microorganisms or by viruses, and as tools for drug development, rational drug
                                                                                                                                                                                    effective amt. of a recombinant human interleukin-3 protein analogue ffective amt. of a recombinant human interleukin-3 protein analogue ribult-3, (Aspl5,Asp70). The rhult-3 analogue has AA SQ in R09326. The compsn. may also comprise the N-terminal octapeptide in R09327, and a diluent and 1 or more than 1 biological response modifier. The compsn. has a biological specific activity of equal to or more than 4.0 x 10 to the 7 mcg/mg in a human bone marrow proliferation assay, and a binding affinity for human monocyte IL-3 receptors of equal to or more equal to or more than 4.0 x 10 to the 10 (M to the minus 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Compsns. contg. recombinant non-glycosylated human interleukin-3 - has increased biological activity and binding affinity, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 97-145687713.

New nucleic acid binding proteins - having an acidic amino acid sequence extension at the amino-terminus, to increase ability to regulate gene transcription, useful e.g. in cancer therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1997 (first entry)
FLAG epitope with nuclear localisation sequence.
PIAG epitope with nuclear localisation sequence.
DNA binding protein; amphipathic peptide;
acidic extension peptide; gene control; gene regulation;
transcription; dominant negative protein; cancer; drug therapy;
drug design; EBP; leucine zipper; FLAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56; DB 3; LA Pred. No. 6.57e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
```

ö

```
US5298395-A.
29-MAR-1994.
                                                                                                                                                                                        Park LŚ;
WPI; 94-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2012

2012

2013

2013

2014

2014

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

2015

        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The state of the s
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-1994 (first entry)
Hyperglycosylated hIL-2 N-terminal fragment.
Human; interleukin-2; IL-2; N-linked carbohydrate; biotinylation; alpha-factor; signal peptide; Zmicron plasmid; detection.
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                            07-JUL-1991 (first entry)
Sequence of a Di-Palmityl Derivatized Identification Peptide.
Hybrid protein; purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                             Score 56; DB 23; Length 13;
Pred. No. 6.57e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 3; Length 13; Pred. No. 6.57e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified site 18.21 /note= "N-linked glycosylation site" Modified_site 22.25 /note= "N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Alpha-factor leader peptide"
CC , design, and drug and gene therapies. So Sequence 13 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "huIL-2 N-terminal fragment"
                                                                                                                                                                                                                                                                                                                    T
P60023 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R46933 standard; Protein; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide 7.15
/note= "Identificaton peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                          Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= palmityl-Lys
Misc_difference 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- palmityl-Lys
EP-195680-A.
24-SEP-1986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc_difference 11
                           13 AA
                                                                                                                                                                                                                    2 dykddddk 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DYKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 dykddddk 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                           P60023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                    RESULT
TD P6
AC P6
DT 07
DE S6
KW HY
FH Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
```

```
Disclosure; 2pp; English.

The sequence is encoded by 4 oligomers. The 8 residue "flag"-DYKDDDDK-
is highly antigenic and provides an epitope reversibly bound by Mab,
enabling rapid assay and easy purificn. of the expressed recombinant hIL-3
The sequence is also cleaved by bovine mucosal enterokinase after the
second Lys. Fusion proteins capped with this peptide are also resistant
to intracclular degradation prior to secretion. DNA encoding fragment
can be used to construct an expression plasmid, pBC125, which can then be
used to transform a yeast expression strain, XV2181, which is cultured
to produce high levels of recombinant hIL-3. The protein can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                 ceil detection method for cells expressing cytokine receptor using hyper:glycosylated recombinant cytokine conjugated to a detectable functional moiety via oligosaccharide residue Example 3; Column 13-14; Bpp; English.

This sequence is encoded by part of a plasmid which was used in the production of a human interleukin-2 (IL-2) protein which has increased levels of N-linked carbohydrate for biotinylation. This sequence spans the Asp718 site at amino acid 79 near the 3; end of the alpha-factor signal peptide to the Spel site in the 2micron plasmid sequence. This polypeptide may be used in the detection method of the invention for the diagnosis of particular physiological or pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purified recombinant human interleukin-3 - used to potentiate immune response or assist in reconstituting normal blood following haematopoietic cell suppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-1990 (first entry)
Fusion protein for expression of hIL-3.
Interleukin-3; fusion protein; yeast; alpha-factor leader; KEX2;
flag peptide;cytopenia; haematopoeisis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 9; Length 27; Pred. No. 6.57e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage_site 14..15
/note=" cleaved by bovine mucosal enterokinase "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=alpha-factor leader
/note=" C-terminal 5 AAs from D718"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-1988.
11-JAN-1988; U00011.
20-JAN-1987; US-004466.
(IMMU-) Immunex Corp.
Anderson DM, Cosman DJ, Price VL;
WPI; 88-22013/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="N-terminal antigenic flag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=identification peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 11
P82355 standard; protein; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
25-APR-1989; 343471.
25-APR-1989; US-343471.
24-JAN-1992; US-827517.
05-NOV-1992; US-972010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=hIL-3 N-terminal WO8805469-A.
                                                                                                                                       (IMMY ) IMMUNEX CORP
                                                                                                                                                                                                      94-100334/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 dykddddk 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DYKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N82115
                                                                                                                                                                                                                                     N-PSDB; Q46933
```

enzyme engineering;

Location/Qualifiers

22..31

S

```
hPSTI.OMTKY3 chimeric subtillsin inhibitor.
Subtilisin inhibitor; protease inhibitor; human; PSTI;
hPSTI.OMTKY3; pancreatic secretory trypsin inhibitor;
turkey ovomucoid third domain protein; enzyme engineeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= OMTKY3
/note= "turkey ovomucoid third domain protein
     .π 13
W26363 standard; Protein; 78 AA.
W26363;
                                                                                                                                                                                                          protein engineering; detergent.
                                                                                                                                                                                                                                  Chimeric Homo sapiens;
Chimeric Meleagris gallopavo;
Chimeric synthetic.
                                                                             02-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                            /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                 /label- Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
     RESULT
                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition(s)

Example 1; Fig 8: 69pp; English.

This sequence comprises human pancreatic secretory trypsin

This sequence comprises human pancreatic secretory trypsin

This sequence comprises human pancreatic secretory trypsin

I is encoded by a DNA construct (see T8452) suitable for

It is encoded by a DNA construct (see T8452) suitable for

Claimed in in which a human standard mechanism inhibitors are

Colaimed in in which a human standard mechanism inhibitor is such as

PSTI, has at least one amino acid (as) of the reactive site

Colaimed in in which a human standard mechanism inhibitor inhibition, for at least one subtilisin, is reduced by at least a factor of 100. Also claimed are: a nucleic acid (I) encoding the

Colaimed in inhibitor; expression vectors containing (I); and host

colls containing (I). The subtilisin inhibitors (see W26362-64)

Combine the low allergenicity of human standard mechanism inhibitors,

which are not specific for subtilisin, and the high affinity of

con-human subtilisin inhibitors. They form a complex with

con-human subtilisin inhibitors. They form a complex with

con-human subtilisin inhibitors. They form a complex with

con-human subtilisin inhibitors of allergenicity in detergent

complex with so as to avoid problems of allergenicity in detergent

configurations, and can also be used in affinity purification and

Sequence 75 AA;
                                                                                                                                                                                                                                       ö
to treat various cytopenias, or can be used in compsns. to potentiate immune response or assist in reconstituting blood cell populations following viral infection or radiation- or chematherapy-induced haematopoletic cell suppression.

See also P82354.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human pancreatic secretory trypsin inhibitor (M2 tagged).
Subtlishin inhibitor; protease inhibitor; PSTI; hPSTI.M2; human;
pancreatic secretory trypsin inhibitor; enzyme engineering;
protein engineering; beculovitus; detergent.
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified subtilisin inhibitor - having altered reactive site resulting in decreased immunogenicity, used in detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56, DB 23; Length 75;
Pred. No. 6.57e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ARRI-) ARRIS PHARM CORP.
Estell DA, Fisher J, Hartman C, McGrath M, Schmidt B; WPI; 97-259023/23.
N-PSDB; T84523.
                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                               Score 56; DB 1; Length 28; Pred. No. 6.57e+00;
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- M2_tag
/note- "facilitates cloning and affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         W26361 standard; Protein; 75 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                               Query Match Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W26361;
2-DEC-1997 (first entry)
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1996; U17153.
25-OCT-1995; US-548186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Homo sapiens;
Chimeric synthetic.
                                                                                                                                  28 AA;
                                                                                                                                                                                                                                                                                    7 dykddddk 14
                                                                                                                                                                                                                                                                                                                 composition(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= hPSTI
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9715670-A1.
                                                                                                                                                                                                                                    .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                       쉱
                                                                                                                                                                                                                                                                                                                                       ŏ
     ឧឧឧឧ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 10A, 69pp; English.

This polypeptide comprises human pancreatic secretory trypsin inhibitor (PSTI), modified to include a turkey ovomucoid third domain (OWTRYI) reactive site. It is encoded by a DNA construct (184525) produced by PCR amplification of overlapping synthetic oligonaleotides. Novel modified subtilisin inhibitors are claimed in which a human standard mechanism inhibitors such as PSTI, has an altered reactive site so that its dissociation constant for inhibition of subtilisin is reduced by at least a constant for inhibitor; expression vectors; and transformed host cubtilisin inhibitor; expression vectors; and transformed host cells. The novel subtilisin, inhibitors combine the low allergenicity of human standard mechanism inhibitors, which are not specific for subtilisin, and the high affinity of non-human subtilisin inhibitors such as OWTKY3. They form a complex with formulations, and can also be used in affinity purification and complex subtilisin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 14 W25364 standard; Protein; 78 AA. W25364 standard; Protein; 78 AA. W26364. Standard; First entry) PSTI.SImutant chimeric subtilisin inhibitor. Brotease inhibitor; human; PSTI; hPSTI.SSI; pancreatic secretory trypsin inhibitor; SSI; enzyme engineering; protein engineering; detergent. Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                               reactive site detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23; Leus.
6.57e+00;
0; Indels
                                                                                                                                                                                                                                     Schmidt B;
                                                                                                                                                                                                                                                                                                         Modified subtilisin inhibitor - having altered resulting in decreased immunogenicity, used in
                                                                                                                                                                              25-OCT-1995; US-548186.
(ARRI-) ARRIS PHARM CORP.
Estell DA, Fisher J, Hartman C, McGrath M,
                                                                               'note= "affinity tag facilitates purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; D
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                      25-OCT-1996; U17153
                                                                                                                                                                                                                                  Estell DA, Fisher WPI; 97-259023/23. N-PSDB; T84525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 dykddddk 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DYKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                                 composition(s)
reactive site<sup>n</sup>
Peptide
                                                    /label= M2_tag
                                                                                                 W09715670-A1.
                                                                                                                                 01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SW KW COT
```

ö

Gaps

ö

Db 🛕 . 68 dykddddk 75

1 DYKDDDDK 8

δλ

ဖ

```
Query Match
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 11A; 69pp; English.

This polypeptide comprises human pancreatic secretory trypsin inhibitor (PSII), modified to include a Streptomyces subtilisin inhibitor (PSII) mutated reactive site. It is encoded by a DNA construct (184526) produced by PCR amplification of overlapping synthetic oligonucleotides. Novel modified subtilisin inhibitors are claimed in which a human standard mechanism inhibitor, such as seconstant for inhibition of subtilisin is reduced by at least a constant for inhibition of subtilisin is reduced by at least a constant for inhibitor; expression vectors; and transformed host cells. The novel subtilisin inhibitors combine the low allergenicity of human standard mechanism inhibitors, which are not specific for subtilisin, and the high affinity of non-human subtilisin so as to avoid problems of allergenicity in detergent constant and can also be used in affinity purification and constant of subtilisin manification and some constant of subtilisin manification and some also be used in affinity purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1997 (first entry)
CMV500-4heptadCREB (New4hepCREB).
CMV500-4heptadCREB (New4hepCREB).
DNA binding protein; RMA binding protein; amphipathic peptide; acidic extension peptide; gene control; gene regulation; transcription; dominant negative protein; CREB; cancer; drug therapy; drug design; CMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                            Modified subtilisin inhibitor - having altered reactive site resulting in decreased immunogenicity, used in detergent
                                                                                                                                                                                                                                                      25-OCT-1995; US-548186.
(ARRI-) ARRIS PHARM CORP.
Estell DA, Fisher J, Hartman C, McGrath M, Schmidt B;
PDT: 9-259033/23.
R-PSDB; T84526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 23; Length 78;
Pred. No. 6.57e+00;
0; Mismatches 0; Indels
                                                                                                           /label- SSI
/label- SSI
/note- "Streptomyces subtilisin inhibitor mutated
reactive site contains Ala at P6, Ala at
P5, Ala at P4, Leu at P1 and Arg at P3'"
                                                                                                                                                                                 /label- M2_tag
/note- "affinity tag facilitates purification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) quantification of subtilisin. 78 AA;
                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W00945 standard; Protein; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
 ◆ Chimeric Streptomyces sp.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric cytomegalovirus;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc_difference 77
/note= "encoded by GAC"
WO9705249-A2.
                                                                                                  22..32
                                                                    Protein 4..78 /label - Mat_protein
                                       Peptide
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-1997.
31-JUL-1996; U12590.
                                                                                                                                                                                                                                          5-OCT-1996; U17153
             Chimeric synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 dykddddk 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DYKDDDDK 8
                                                                                                                                                                                                                                                                                                                                                            composition(s)
                                                                                                                                                                                                             709715670-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (diagnostic)
                                                                                                                                                                                                                             -MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W00945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    éy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                      regulate gene transcripton, useful e.g. in cancer therapeutics claim 16; Page 83-84; 144pp; English.

This sequence comprises the polypeptide CMV500-4heptadCREB, or New4hepCREB, which has a 4heptad appended acidic extension.

Claimed nucleic acid binding proteins (NABPS) such as CREB that have acidic peptide extensions are capable of regulating the function of a target nucleic acid or gene to which they are bound, and act as potent dominant negative regulators of gene transcription, cell growth and cell proliferation. They can be used in cancer therapeutics, to treat diseases caused by eukaryotic microorganisms or by viruses, and as tools for drug development,
                                                                                                                                                                                                                                                                                                           New nucleic acid binding proteins - having an acidic amino acid sequence extension at the amino-terminus, to increase ability to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rational drug design, and drug and gene therapies. They have an extended protein interaction surface or multimerisation or dimerisation interface that increases the stability of complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 23; Length 84;
Pred. No. 6.57e+00;
0; Mismatches 0; Indels
                                                                                                    (KRYL/) KRYLOV D.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(VINS/) VINSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: Tue Feb 3 15:33:16 1998 Job time: 18 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                      31-JUL-1995; US-001654.
29-MAY-1996; US-018496.
31-JUL-1996; US-001654
31-JUL-1995; US-001654
                                                                                                                                                                                                      Krylov D, Vinson CR;
WPI; 97-145687/13.
N-PSDB; T84345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 dykddddk 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DYKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
```

ö

SUMMARIES

98:EST294

measure.Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, measure.and.is derived by analysis of the total score distribution.

Mean 10.704; Variance 4.122; scale 2.597

Statistics:

```
Homo sapiens
                                                                                                                                                                                                                                                  240 tttaatga 247
                                                                                                                                                                                                                                                                                 130 ATGTATGA 137
                                                                                                                                                                                                                                                                                                                                                                                                    q1813189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153
                                                                   185
                                                                                                                                                                                                                                                                                                                                                                                                                                    uman.
                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                   BASE COUNT
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                  RESULT
LOCUS
                                                                                   ORIGIN
                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                 ò
                                                             Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Ragasuno Rawauchi-cho, Tokushima, Tokushima, 771-01, Japan (Tel:0886-65-2888, Fax:0886-37-1035) Submitted (30-May-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST(expressed sequence tag).
Rattus norvegicus rat pancreatic islets cDNA to mRNA, clone_lib:Rat
pancreatic islet cDNA clone:RBC865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Large scale collection of expressed sequence tags (ESTs) from rat pancr eatic islet cDNA library Unpublished (1996)
2 (bases 1 to 506)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA was prepared from normal rat islets. cDNA was directionally synthesized from the Xho I in the vector to the EcoRI site. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-JUN-1996) to the DDBJ/EMBL/GenBank databases. Jun Takeda, Institute for Molecular and cellular Regulation.Gunma University, Dept. of Molecular Medicine; 3-39-15 Showa-machi, Maebashi 371, Japan (E-mail:jtakeda@new.sb.gunma-u.ac.jp, Tel:81-272-20-8855, Fax:81-272-20-8895)
Project='Rat pancreatic islet cDNA'
vector-Lambda ZAPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Clontech human fetal brain polyA+ mRNA (#6535)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 104; Length 362;
                                                                                                                                                                                                                                                                                                                                                                                   10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 104;
Pred. No. 4.53e-04;
5; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
                                                                                                                                            Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 kagasuno Kawauchi-cho
Tokushima, Tokushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 56 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  506 bp
                                                                                                                                                                                                                                                                                                                                                                                                                               h 6.0%;
Similarity 62.5%;
45; Conservative
Unpublished (1995)
2 (bases 1 to 362)
                                                                                                                                                                                                                                                                 Phone: 0886-65-2888
                                                                                                                                                                                                                                                                                 : 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                 88
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to none.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer-T7 primer
                                                                                                                                                                                                                                                                                                               1..362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 aaaaaaaaaa 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 AAAATGAAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rsitel-Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rsite2-Xho I
                         fujiwara,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (sites)
                                                                                                                                                                                                                                                                                                                                                                                   ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91503948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rakeda, J
                                                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C07172
                                                                                                                                                                                                                                                  Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL
REFERENCE
AUTHORS
                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
```

유 õ 셤 ð .7

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Enail: est@watson.wustl.edu
This clone is available royalty-free through LLNL: contact the IMGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1129 Std Error: 0.00
Seq primer: -41m13 fwd. Er from Amersham
                                                                                                                                                                                                                                                        AA214564 535 bp mRNA EST 19-MAY-1997 zr92e05.s1 Soares NbHTGBC Homo sapiens cDNA clone 683168 3'. AA214564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 535),
Hilliari,. Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hilliar,L., Clark,N., Elliston,G., Marra,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohliing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Washt-Merck EST Project
Wablished (1995)
                                                                                                                                                                                                           ö
                                                                                                                                                         Score 28; DB 91; Length 506;
Pred. No. 4.53e-04;
0; Mismatches 20; Indels
/organism="Rattus norvegicus"
/clone="REO865"
/clone_lib="Rat pancreatic islet cDN:
/tissue_type="rat pancreatic islets"
68 c 63 g 190 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares NbHTGBC"
/tissue_type="Germinal B-cell"
/lab_host="DH10B"
complement(<1..>5335)
/db_xref="GDB:5586488"
a 123 c 101 g 151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                              Query Match 6.0%;
Best Local Similarity 70.6%;
                                                                                                                                                                                                             Conservative
```

US-08-713-928A-5.rstb

```
260 ACTCCATTCAAAATATAAAATGAAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||| ·||||||
TTTTAATTTTT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttttttttttt 235
                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                  DEFINITION
                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
BASE COUNT
                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224
                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                             ACCESSION
                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                   COMMENT
                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                             NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Сp
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                       Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA254732 231 bp mRNA EST 14-MAR-1997 m280004.rl Soares mouse NML Mus musculus cDNA clone 719767 5' similar to gb:M31131 Mouse neural cadherin (MOUSE);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 34; Length 231; Pred. No. 1.17e-02;
            Length 535
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 211.
Location/Qualiflers
           Score 27; DB 97;
Pred. No. 2.34e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="719767"
/clone_11b="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH108"
                                                               224 AAAAAAAAAGAAAGTATATTATTGTAAAAGATAA 258
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 t
                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 aaaaaaaaaaaaaaaaaaaaaaaa 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.6%;
         5.8%;
Similarity 88.6%;
31; Conservative
                                                                                                                                                                                                                                                                                                  (bases 1 to 231)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo.
                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:445263
                                                                                                                                                                                                       g1889317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                     Mus.
           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                   RESULT
                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
Murinae; Mus.
1 (bases I to 243)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescribe (modified); Site_1: Mlu1; Site_2: Sal1; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: Sal1(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTT3'. CDNAS were cloned into the Mlu1/Sal1 sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA243996 327 bp mRNA EST 10-MAR-1997 nc05a05.rl NCI CGAP Pr1 Homo sapiens cDNA clone 1353 similar to AA243996 shown Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:470894
Ve50904.r1 Knowles Solter mouse 2 cell Mus musculus cDNA clone AA414924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||| ||||| |||| ||||| ||||| |||| |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26; DB 67; Length 243;
Pred. No. 1.17e-02;
0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Knowles Solter mouse 2 cell"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 137.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(<1..>243)
26 c 35 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="B6D2 F1/J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.6%;
Best Local Similarity 68.1%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/organism="Homo sapiens"
/note="Vector: pAMPI0; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCNA applied to the
cDNA with an adaptor-specific primer, and the resulting
PCN product subcloned into pAMPI0 by the UDG-cLoning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 342)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA271298 342 bp mRNA EST 26-MAR-1997
VA73a07.r1 Soares mouse 3NWE12 5 Mus musculus cDNA clone 762612 5'
91909627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 327)
1111acr,L., Allan,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Marra,M., Martin,J.,
White,Y., Wylie,T., Waterston,R. and Wilson,R. Theising,B.,
WashU-NCI EST Project
                                                                                                                                                                                                                                                                                                                                                                                     This clone is available from the NCI; contact David B. Krizman, Ph.D. (dkrizman@nchgr.nih.gov) for further information. Seq primer: -28ml3 rev1 Er from Amersham High quality sequence stop: 116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                 Contact: Wilson RK / WashU-NCI EST Project
WashU-NCI EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 13; Length 327;
Pred. No. 1.17e-02;
0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI CGAP Prl"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
9
                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 68.1%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 C
                                                                                                                                                                                                           Unpublished (1996)
                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 ttttttttttt 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 TTTTAATTTTT 216
                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ๗
                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                           JOURNAL
                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
KEYWORDS
                                                                                                                                                                                     ATITLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c<sub>D</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           윱
```

```
ö
                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         дадэл149 408 bp mRNA EST 12-MAR-1997
2804e04.s1 Soares NbHTGBC Homo sapiens cDNA clone 684222 3'.
AA251149
91886131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 408)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                           Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 47; Length 342; Pred. No. 1.17e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="762612"
/clone_lib="Soares mouse 3NME12 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 283. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 AAGATAATACTCCATTCAAAATATAAAATGAAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 t
                                                           Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match
Local Similarity 63.5%;
nes 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 c
                                                                                                     Unpublished (1996)
                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <1..>342
                                                                                                                                                                                                                                                                                                                                                                                                                    1..342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                               MGI:463532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
```

S

```
Query Match
Best Local Similarity {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92045187
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                              BASE COUNT
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (09-APR-1997) to the DDBJ/EMBL/GenBank databases. Hideko Urushihara, University of Tsukuba, Institute of Biological Sciences; 1-1-1 Tennohal, Tsukuba, Ibaraki 305, Japan (E-mail:d402hu@sakura.cc.tsukuba.ac.jp, Tel:0298-53-4664,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (strain:KAX3) Sexually competent gamete CDNA to mRNA, clone_lib:FCL.
Dictyostelium discoideum
Eukaryotae; mitochondrial eukaryotes; Dictyosteliida;
                Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest 1810
-Emarky-westewatson.wustl.edu

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructed by Bento Soares and M. Fatima Bonaldo. /clone="68422"
/clone_lib="Soares NbHTGBC"
/tissue_type="Germinal B-cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sexual cDNA in CSM
Unpublished (1997)
PROJECT = 'Dictyostellum discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C23818 513 bp mRNA EST 22.
Dictyostelium discoideum gamete cDNA, clone FCL-AB12.
C23818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 ATAAAACTITACTICAAAAATTAAAAAAAAAAAAAGAAAGTATATI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 atatatattttattataaaatagaaaaaaaaaaagtatatt 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Dictyostellum discoideum"
/strain="KAX3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (sites)
Kobayashi,A., Shimizu,H. and Urushihara,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 23; I
Pred. No. 1.17e-02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(<1..>408)
54 c 64 a
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="gamete"
/clone_lib="FCL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST(expressed sequence tag)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%;
llarity 79.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ax:0298-53-6614)
                                                                                                                                                                                                                                                                                                                                                     1..408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urushihara, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g2073330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D
YWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                      FEATURES
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
1..746
Acoganism="Drosophila melanogaster"
/note="Organ: embryo; Vector: BlueScript SK: Site_1:
EcoRI; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis Kit. Oligo dT-primed and directionally cloned at
EcoRI and XhoI in BlueScript SK(+/-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Bmail: EST@fruitfly.berkeley.edu, http://fruitfly.berkeley.edu/
Based upon the presence of a run of 10 or more T residues in the
first 30 bases of the read this clone possibly contains an inverted
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mn83f05.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone 250689 5'.
AA096579
91644156
                                                                                                                                                                                                                                                                        AA392077 746 bp mRNA EST 24-APR-1997
CLD1555.5prime LD Drosophila Embryo Drosophila melanogaster CDNA
AA392077
                                                                                                                                                                             412 aaattacttttttattattaatattgcaaaaattattataataattgattatttaaatta 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Eukaryotae; mitochondrial eukaryotes; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 746)
Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Brokstein,P., Lewis,S. and Rubin,G.M.
Unpublished (1997)
                                                                                                                                                                                                                      98 AAAGTAGATATTAAAATTTTGAAATATCAGTTTAATAATTGGTTATAATTG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="LD Drosophila Embryo"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="Xil Blue MRF"
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                        Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 746;
                                                                                  Score 26; DB 68; Length 513
Pred. No. 1.17e-02;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 64; Ler
Pred. No. 1.17e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Sexually competent"
58 c 60 g 178 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insert
Plate: 115 row: E column: 7
High quality sequence stop: 580.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 g
                                                                                                                                                                                                                                                                                                                                                                                                                                          fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.6%;
llarity 82.5%;
Conservative
                                                                                    y Match 5.6%;
Local Similarity 71.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <1..>746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Harvey, D.
                                                                                                                                  43; Conservative
```

KEYWORDS SOURCE

REFERENCE

AUTHORS

THE SECTION

```
Submitted (04-APR-1997) to the DDBJ/EMBL/GenBank databases. Hideko Urushihara, University of Tsukuba, Institute of Biological Sciences; 1-1-1 Tennohdai, Tsukuba, Ibaraki 305, Japan (E-mail:4402hu@akura.cc.tsukuba.ac.jp, Tel:0298-53-4664,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST(expressed sequence tag).

Dictyostelium discoideum (strain:KAX3) Sexually competent Gamete CDNA to mRNA, Clone_lib:FC.
Dictyostelium discoideum
                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Dictyostellida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C23711 224 bp mRNA EST 2.2
Dictyostelium discoideum gamete cDNA, clone FC-AB09.
C23711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Indels
                                                                                                Washu-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (sites)
Kobayashi,A., Shimizu,H. and Urushihara,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="unknown"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                          Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 98. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 5.63e-02;
0; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ىد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                               Contact: Marra M/Mouse EST Project
Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 aaaaaaaaaaaaaaaaaaaaaaaa 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 CCATTCAAAATATAAAATGAAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%;
Best Local Similarity 64.7%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 C
                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urushihara, H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                    1..184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium.
                                                                                                                                                                                                                                                                       MGI:412028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q2073223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhoi; Cloned unidirectionally. Primer: 011go dr. M30 CD4+
cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5.
adaptor sequence: 5 GAATTCGGCACAGG 3 -3 adaptor
sequence: 5 CTCGAGTTTTTTTTTTTTTTTTT 3."
                                                                                                                   1 (bases 1 to 127)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Tabeasangy&www.Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA231547 184 bp mRNA EST 26-FEB-1997 mw31e07.rl Soares mouse 3NWE12 5 Mus musculus CDNA clone 672324 5' similar to gb:X07315 PLACENTAL PROTEIN 15 (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          th LLNL; contact the further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                     Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                            Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene mouse Tcell 937311"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 16; Length 127
Pred. No. 5.63e-02;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 110.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 t
                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="550689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.4%;
larity 64.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 55; Conser'
                   nouse mouse.
                                                                                                                                                                                                                              Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:331481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91853854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus.
                                                                                                    Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
BASE COUNT
ORIGIN
                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                             TITLE

JOURNAL

COMMENT
```

FEATURES

.0

Gaps

ö

22-APR-1997

ACCESSION

g

셤

KEYWORDS

SOURCE

AUTHORS

REFERENCE

```
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96026280
                                                                   152
                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                         RESULT
LOCUS
                                                                                  ORIGIN
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                           원
                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA266722 247 bp mRNA EST 21-MAR-1997 mG8f06.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone 721475 5'.
AA266722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                         Gaps
Sexual cDNA in CSM
Unpublished (1997)
PROJECT - 'Dictyostellum discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares mouse lymph node NbMLN"
                                                                                                                                                                                                          Length 224;
                                                                                                                                                                                                                                          0; Mismatches 34; Indels
                                                                               /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                               competent"
53 t
                                                                                                                                                                                                          Score 25; DB 68;
Pred. No. 5.63e-02;
                                                                                                                                                                                                                                                                                                                                      159 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 191
                                                                                                                                                                                                                                                                                                                                                                     255 ATAATACTCCATTCAAAATATAAAATGAAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 206.
Location/Qualifiers
                                                                                                                                            dev_stage="Sexually
11 c 11 q
                                               Location/Qualifiers
                                                                                                            /cell_type="Gamete"
/clone_lib="FC"
                                                                                                                                                               b
                                                                                               /strain="KAX3"
                                                                                                                                                                                                         Query Match 5.4%;
Best Local Similarity 63.4%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Per 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:446971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91903564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus.
                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
 TITLE
JOURNAL
                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
```

ŏ

```
l (Jagas, M.D., Kerlavage, A. R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Frandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhudp, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M., Moreno-Palaques, R.E., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarlik, D.P., Cao, L., Cepeda, M.A., Coleman, T.R., Collins, E.J., Dimke, D., Ferry, Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hunglun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fistser, C.K., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA303340 253 bp mRNA EST 18-APR-1997
EST15962 Aorta endothelial cells Homo sapiens cDNA 5' end similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                         /note="Otgan: aorta; Vector: pBluescript SK-; Site_1:
BcoRI, Site_2: XhoI"
/clone_lib="Aorta endothelial cells"
/cell_type="endothelial cell"
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                            Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                  Score 25; DB 45; Length 247
Pred. No. 5.63e-02;
0; Mismatches 30; Indels
                                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to EST containing Alu repeat.
AA303340
g1955694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                           p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 aaaaaaaaaaaaaaaaaaaaa 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 CCATTCAAAATATAAAATGAAAAA 287
                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
                                                                                                                                                                                                     Query Match 5.4%;
Best Local Similarity 64.7%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: THC97352
                                                                                                 20 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
```

```
1 others
                 58 t
               59 g
/dev_stage="adult"
<1..>253
91 a 44 c 59 g
    mRNA
BASE COUNT
ORIGIN
```

0; Gaps Query Match 5.4%; Score 25; DB 27; Length 253; Best Local Similarity 83.8%; Pred. No. 5.63e-02; Matches 31; Conservative 0; Mismatches 6; Indels

ó

δ q

Search completed: Tue Feb 3 20:14:24 1998 Job time: 488 secs.

b

```
1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8 1:STS2 1:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8 9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:GDEST1 15:GDEST2 16:GDEST3 17:GDEST4 18:GDEST3 19:GDEST6 20:GDEST6 20:GDEST7 21:GDEST8 22:GDEST4 23:GDEST10 24:GDEST11 25:GDEST1 24:GDEST11 25:GDEST13 24:GDEST13 24:GDEST13 24:GDEST13 24:GDEST13 25:GDEST2 25:GDEST3 25:GDEST2 25:GDEST3 25:GDEST3 25:GDEST3 25:GDEST2 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAATACGATATTACCGAATA.......CGGTGAAAGTAAGGGGGTC 463
GTTATGCTATAATGGCTTAT........GGCCACTTTCATTCGTCWAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tue Feb 3 20:14:46 1998; MasPar time 150.66 Seconds 775.329 Million cell updates/sec
(MI)
                                                                                                                                                                                                                                                                                                                                                             - n.a. database search, using Smith-Waterman algorithm
                                                                                                                                                                         Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333433 seqs, 126143548 bases x 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               >US-08-713-928A-5
(1-463) from US08713928A.seq
463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dbase 0; Query 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TABLE default
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not generated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gap 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                      n.a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Description:
Perfect Score:
N.A. Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abular output
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nmatch STD
                                                                                                                                                                                                                                                                                                                                                        MPsrch_nn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
```

Mean 10.998; Variance 4.755; scale 2.313 statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.32e-03 1.32e-03
114	falciparum 1 falciparum 1
eswlt Query No. Score Match Length DB ID Description Pred. No.	Plasmodium falciparum 1.32e-03 Plasmodium falciparum 1.32e-03
ID	488 94 PFAF10513 488 45 AF010513
* Swit Query No. Score Match Length DB ID	488 94 488 45
Query Match I	6.3
Score	700
Result No.	0 0 7

.75e- .75e- .44e- .44e- .44e- .44e-		900000000000000000000000000000000000000			
um di Knowl Knowl Osome Osome HGC-9 Soare	zr92e05.s1 NCI_CGAP_G nh05c07.s1 NCI_CGAP_T n989c07.s1 NCI_CGAP_P ng89c07.s1 NCI_CGAP_P ng89c07.s1 NCI_CGAP_P Dictyostelium discoid nco5a05.r1 NCI_CGAP_P nc05a05.r1 NCI_CGAP_P	NCJ NCJ NCJ NCJ Seb	nc66d05.s1 NCI_CGAP_P ad68901.s1 NCI_CGAP_G ad68901.s1 NCI_CGAP_G zu45b01.s1 Scares ova nc60b12.s1 NCI_CGAP_P systcopy.s1 NCI_CGAP_G zs9zdog.s1 NCI_CGAP_G zsyzdog.s1 NCI_CGAP_G zsyzdog.s2 NCI_CGAP_G zsyzdog.s2 NCI_CGAP_G zsyzdog.s2 NCI_CGAP_G zsyzdog.s2 NCI_CGAP_G zsyzdog.s2 NCI_CGAP_G	rsion 1) A28 sequence. e) Alveolata; Apicomplexa;	alciparum linkage map: imple sequence repeats" nBank/DDBJ databases.
111 111 12933 12933 12933 104 104	664 1157 145 145 145 1996 196	49 877 1271 1909 161 1077 1388 1388	AA470491 AA521334 HS131234 AA520433 HS1270075 AA20493 HS121334 MM1267001 HS1322012 HS1184115 AA279725 C24618	ALIGNMENTS STS, 488 BP. ated) t updated, Veri rosatellite TA. laria parasite eukaryotes; A.	re D
44844 887	10004447	HU4044640C	884 26 994 411 995 44 11 995 99 74 995 996 997 995 996 996 997 996 997 997 997 997 997 997 997 997 997 997	ONA; Cre Las mic (ma	on f t as
R004444R		4400010000		dard; 1.52 1.52 iparu iparu ochom	மைய் மட்டுக
			លេលលលលលលលលលលល ភ.ភ.ភ.ភ.ភ.ភ.ភ.ភ.ភ.ភ.ភ.ភ. ភ.	st ((fa	ell c m 3:4 8:4 ell
2222 2222 2222 2222 2222 2222 2222 2222 2222	22222222222222222222222222222222222222	12222222222222222222222222222222222222	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	PPAF10513 AF010513; 92253505; 14-JUL-1999; 14-JUL-1999; Plasmodium Plasmodium Plasmodium Eukaryotae,	
110 110 110 110	12 114 114 117 118	000000000000000000000000000000000000000		5	1-4 Su TO PO Gen (Gen (2) 1-2) Sub NIA NIA KEY
υυ	0000 00	ο οοο	000000	RE DE DE SE	RA REL RET

```
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                       STATESTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C (bases 1 to 488)
Su.X.z. and Wellems, T.E.
Su.M.z. and Wellems, T.E.
Su.M.z. and Wellems, T.E.
Submitted (27-JUN-1997) NIAID-Laboratory of Parasitic Diseases,
NIH, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
-Bukarayeeteg-wmtrochondrial eukaryotes; Alveolata; Apicomplexa;
Haemosporida; Plasmodium.
1 (Dases 1 to 488)
Su, X. z. and Wellems, T. E.
Toward a high-resolution Plasmodium falciparum linkage map:
polymorphic markers from hundreds of simple sequence repeats
Genomics 33 (3), 430-444 (1996)
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1997) to the EMBL/GenBank/DDBJ databases.
Hideko Urushihara, University of Tsukuba, Institute of Biological
Sciences; Ten-noudai 1-1-1, Tsukuba-shi 305, Japan
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                               Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF010513 488 bp DNA STS 1
Plasmodium falciparum microsatellite TA28 sequence.
RF010513
92253505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 488;
                                                                                                                                                                           Score 29; DB 45; Length 486
Pred. No. 1.32e-03;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                         260 TAITATCTITIACAATAATAIACITICTITITITITITATITITI 216
                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Dictyosteliida;
Dictyostelium.
                                                                                                                                            BP; 182 A; 69 C; 37 G; 200 T; 0 other;
                            /organism="Plasmodium falciparum"
/chromosome="6"
1..488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Plasmodium falciparum"/chromosome="6"
1..488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1997 (Rel. 52, Created)
26-JUL-1997 (Rel. 52, Last updated, Version 1)
Dictyostellum discoldeum slug cDNA, clone SSA892.
EST(expressed sequence tag).
Dictyostellum discoldeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"microsatellite TA28"
69 c 37 g 200 t
                                                                                                                       note-"microsatellite TA28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25057;
225657;
d1112191
                                                                                                                                                                                          Query Match 6.3%;
Best Local Similarity 82.2%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.3%;
Best Local Similarity 82.2%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malaria parasite.
                    1..488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96299638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Urushihara H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                             repeat_region
                                                                                                                                              Sequence 488
FT : source
FT :
FT repeat_;
FT t
                                                                                                                                                                                                                                                                                                                                                                                                                               ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT

1D DD

1
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                 ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Сp
```

```
Murinae; Mus.

1 (bases 1 to 607)

Martra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Martra,M., Hillier,L., augy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.linl.gov) for further information. MGI:521064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               607 bp mRNA EST 17-JUL-1997
Knowles Solter mouse E6 5d whole embryo Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
6.0%; Score 28; DB 46; Length 506;
Best Local Similarity 67.5%; Pred. No. 5.75e-03;
Matches 54; Conservative 0; Mismatches 26; Indels
                                                                                                                                              PROJECT - "Dictyostellum discoideum cDNA project in Japan"
                                                                      Saitch T., Morio T., Tanaka Y., Ochiai H.;
"Developmental cDNA in Dictyostelium discoideum(970723)";
Unpublished.
(E-mail:qxurushi@bank.dna.affrc.go.jp, Tel:0298-53-4664,
Fax:0298-53-6614)
                                                                                                                                                                                                                  1..506
/clone_lib="SS"
/dev_stage="Slug"
/dev_granism="Dictyostellum discoideum"
/sequenced_mol="cDNA to mRNA"
/strain="AX4"
55 BP; 238 A; 63 C; 63 G; 142 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..607
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 356.
Location/Qualifiers
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 taaaataaaaaaaaaaa 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||| |||| ||||| |||||| 268 CAAAATATAAAATGAAAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vh78c09.rl Knowles concount clone 893104 3'. AA522011 92262756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA522011
                                                                                                                                                                                                                                                                                                                                                                     Sequence 506
                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
```

```
Presoak: 0 degrees C for Denaturation: 92 degrees C for Annealing: 55 degrees C for Polymerization: 72 degrees C for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                each 1 um
each 200 um
0.05 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR Cycles: 35
Thermal Cycler: PerkinElmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-100 ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..245
/organism="Homo sapiens"
/map="7"
24..185
24..41
                                                                                                                                                                             HUMSWS2933 245 bp DNA
human chromosome 7 STS SWSS2933.
G16157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 7 (1), 59-64 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5 mM
100 mM
10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 ⊞M
8.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer A: TCAACATCTTCAACAGAC
Primer B: AGTGTGAATGTTTGATGG
STS size: 162
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smail: egreen@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human chromosome 7 STSs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taq Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Eric D. Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 245)
                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCl:
Tris-HCl:
NH4Cl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            remplate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDB: GDB:1318428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MqC12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dNTPs:
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green, E.D.
                                                                                                                                                                                                                                                                    q1185334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97189344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buffer:
                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
                                                                                                                                                                        ဖ
                                                                                                                                                                                                                     DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                        RESULT
                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="B6D2 F1/J"
/note="Vector: pBluescribe (modified); Site_1: MluI;
/note="Vector: pBluescribe (modified); Site_1: MluI;
Site_2: SalI; Cloned unidirectionally from mRNA prepared
from 13,500 2-cell stage embryos. Primer: SalI(dT):
5'-CGGTCGACCGTTTTTTTTTTTTTT"3'. CDNAs were cloned
into_the MluI/SalI sites of a modified pBluescribe vector
using commercial linkers (NEB)."
                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                               /clone_lib="Knowles Solter mouse E6 5d whole embryo"
/dev_stage="embryo (post-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="893104"
/clone_lib-"knowles Solter mouse E6 5d whole embryo"
/dev_stqe="embryo (post-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mousesst@watson.wustl.edu This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.iln.gov) for further information. MGI:521064 High quality sequence stop: 356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubdque T., Galsel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-1997 (Rel. 52, Created)
18-JUL-1997 (Rel. 52, Last updated, Version 1)
vh78c09.11 Knowles Solter mouse E6 5d whole embryo Mus musculus
CDNA clone 893104 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                   Length 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 88; Length 607
Pred. No. 5.75e-03;
0; Mismatches 34; Indels
                                                                                                                                                                 Score 28; DB 41; Length 607
Pred. No. 5.75e-03;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                complement(<1..>607)
266 A; 96 C; 108 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                        complement(<1..>607)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The WashU-HHMI Mouse EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ULT 5
MM1313659 standard; RNA; EST;
                                                                                                                                                                 Similarity 66.0%; 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.0%;
Best Local Similarity 66.0%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 607 BP;
                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA522011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RITER S FIRE S F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ୍ ନୁ
                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F., Wachtraub, L.A., Whrr-Tidwell, R.M., Peluso, D.C., Fulton, R.S., Leckle, M.P. and Green, E.D. A collection of 1814 human chromosome 7-specific STSs
                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Technology Erzarch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014022011
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence for this STS was derived from a single seque read. For additional information about the NHGRI chromosome mapping project, see http://www.nhgri.nih.gov/DIR/GTB/CHR7.see Genomics 11:548-64 (1991) [MUID=92128937].
02-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.00 minute(s)
0.17 minute(s)
1.00 minute(s)
1.00 minute(s)
                                                                                                                                           STS sequence; primer; sequence tagged site
```

ö

Gaps

ö

06-0CT-1995

human.

SOURCE

KEYWORDS

DEFINITION

ą ò ACCESSION

HOMO.

REFERENCE

AUTHORS

TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL COMMENT

```
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata;
Tetrapoda; Amilote; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       FIS Sequence; primer; sequence tagged site.

human Plasmid clones, generated from a lymphoblastoid cell line
from a human male. Localized to human chromosome 1 by analysis on
the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell
Institue for Medical Research, Camden, NJ 08103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                           Query Match 5.8%; Score 27; DB 12; Length 245; Best Local Similarity 93.5%; Pred. No. 2.44e-02; Matches 29; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 degrees C for 15 s
62 degrees C for 23 s
72 degrees C for 30 s
30
Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                        SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 ng
each 1 uM
each 200 uM
0.05 units/ul
10 ul
                                                                                                                                            ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer A: GTTTACTAGATGATGCTAACCACG
Primer B: TGTGTATCTCCCCGACAGAGT
STS size: 280
PCR Profile:
                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                      G11046 400 bp DNA
human STS SHGC-9031 clone pG-4789.
G11046
                                                                                                                                                                                                                                                               1..245
/organism="Homo sapiens"
                                                                  /map="7"
24.185
24.41
complement(168.185)
a 37 c 29 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     죝죝죝
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.5 I
50 I
20 B.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosome 1.
Location/Qualifiers
1..400
                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annealing:
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR Cycles:
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              raq Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCl:
Tris-HCl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Template:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MgC12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dNTPs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                          122 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers, R.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                          9988152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buffer:
                                                                                                          primer_bind
                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                         source
                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                        NID
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                          SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                     FEATURES
                                                                                                                                          BASE ĈO
ORIGIN
                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 245)
Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F.,
Bouffard, G.G., Iyer, L.M., Mohr-Tidwell, R.M., Peluso, D.C., Fulton, R.S.,
Leckie, M.P. and Green, E.D.
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhin; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ===#Rhas=soquence-for this STS was derived from a single sequentead. For additional information about the NHGRI chromosome mapping project, see http://www.nhgri.nih.gov/DIR/GTB/CHR7. see Genomics 11:548-64 (1991) [MUID-92128937].
                                                                                                                                                                                                                                                                 02-APR-1997
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.00 minute(s)
0.17 minute(s)
1.00 minute(s)
1.00 minute(s)
                                                                                                                          ö
                                                                                      Length 245;
                                                                    Score 27; DB 11; Length 243.
Pred. No. 2.44e-02;
                                                                                                                                                                                                                                                                   SIS
                                                                                                                                                                                                                                                                                                                  g1185334
STS sequence; primer; sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 degrees C for
92 degrees C for
55 degrees C for
72 degrees C for
35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR Cycles: 35
Thermal Cycler: PerkinElmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-100 ng
each 1 uM
each 200 uM
0.05 units/ul
10 ul
                                    57 t
                                                                                                                                                                            213 TTCAAAAATTAAAAAAAAAAGAAAGTATAT 243
                                                                                                                                                          114 tttaaaaaattaaaaaaaaaacaaagtatat 144
                                                                                                                                                                                                                                                   HUMSWS2933 245 bp DNA
human chromosome 7 STS SWSS2933.
G16157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5 mM
100 mM
10 mM
5 mM
8.6
                  complement(168..185)
a 37 c 29 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer A: TCAACATCTTCAACAGAC
Primer B: AGTGTGAATGTTTGATGG
STS size: 162
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: egreen@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Denaturation: 9
Annealing: 5
Polymerization: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDB: GDB:1318428
Contact: Eric D. Green
Genome Technology Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dNTPs:
Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human chromosome 7 STSs
Unpublished (1997)
                                                                                    Owery Match 5.8%;
Best Local Similarity 93.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        remplate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tris-HCl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Presoak:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MgC12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NH4C1:
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
primer_bind c
BASE COUNT 122 a
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97189344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buffer:
```

```
Mus musculus
                                                                                                                                                                                                                                                                                                                                               house mouse.
                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     AA510004
vh53d10.r1 8
890707 5'.
AA510004
                                                                                                                                                                                                                                                                                                               g2247858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132
                                                                                                                                                              153 ttt 155
                                                                                                                                                                                            226 TTT 224
                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE .
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                         Matches
                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                  NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                a
                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by Dr. Minoru Ko, Wayne State Univ. Library constructed an
                                                                                                                                                                               ö
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                            . იმგაუცე - გამმოდებდები Created)
09-JUL-1997 (Rel. 52, Last updated, Version 1)
vh53d10.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through Linl.; contact the IMAGE Consortium (info@image.lln.gov) for further information. MGI:518667 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               normalized by Bento Soares and M.Fatima Bonaldo."

/clone="890707"

/clone="1b="Soares mouse mammary gland Nbhwg"
/sex="male"
/fissue_type="mammary gland"
/dev stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>د</u>
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson
                                                                                                                                                                               ö
                                                                                                      others
                                                                                                                                    Score 27; DB 4; Lengum +vv., Pred. No. 2.44e-02; ....matches 6; Indels
                                                                                                     56
                                                                                                                                                                                                           gagtatatgaaactttacttagaaaaaaaaaaaaaaa 152
                                                                                                                                                                                                                        109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
sapiens
                                                                                                                                                                                                                                                                                                  BP
                                                                       complement(346..366)
/map="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The WashU-HHMI Mouse EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                      б
                                                                                                                                                                                                                                                                                   FULT 9
MM1303648 standard; RNA; EST; 441
MM2510004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
                                                                                                      62
/organism="Homo
87..366
                                                                                                                                               Query Match 5.8%;
Best Local Similarity 84.6%;
Matches 33; Conservative
                                                                                                   71 c
                                         87..111
/map="1"
                             /map="1
87..111
                                                                                                      ಡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae; Mus.
                                           primer_bind
                                                                     primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                         890707 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                     COUNT
                                                                                                                                                                                                           114
                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                              굺
```

```
441 bp mRNA EST 08-JUL-1997
Soares mouse mammary gland NbMMG Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepto, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                286 ITITICATITITATATITIGAAIGGAGIATIATCITITACAAIAAIAIACITICITITITI 227
                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="890707"
/clone_lib="Soares mouse mammary gland NbMMG"
/sex="male"
                                                            Length 441;
                                                         Score 27; DB 86; Length 441
Pred. No. 2.44e-02;
0; Mismatches 18; Indels
mRNA <1..>441
Sequence 441 BP; 132 A; 53 C; 84 G; 172 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOI:518667
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 397.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="4 weeks"
/lab_host="DH10B"
<1..>441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                            h 5.8%;
Similarity 71.4%;
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murinae; Mus.
```

'n

```
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1129 Std Error: 0.00 Seq primer: -41m13 fwd. Err from Amersham High quality sequence stop: 275.
zr92e05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 683168
AA214564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 AAAAAAAAAGAAGTATATTATTGTAAAAGATAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 aaaaaaaaaagacagtattttattgtaatatataa 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(<1..>535)
/db_xref="GDB:5586488"
123 c 101 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS1284157 standard; RNA; EST; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%;
88.6%;
                                                                                                                                                                   (bases 1 to 535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                     NCI-CGAP.
                                      q1813189
                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA493647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q2223488
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Source
DEFINITION
ACCESSION
                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                        AUTHORS
                                                                                                                                                                   REFERENCE
                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." /clone="683168" /clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Eco RI sites of the modified pT7T3 vector. Library wen
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                      286 TITITCATITIATATITIGAAIGGAGTATIAICTTITACAATAATATACTTICTTTTT 227
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
Robert Strausbergenih, gov This clone is avallable royalty-free
Abrough LINL; contact the IMAGE Consortium (infoelimage.llnl.gov)
for further information. Insert Length: 1129 Std Error: 0.00 Seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                g1813189
03-FEB-1997 (Rel. 50, Created)
16-JUM-1997 (Rel. 52, Last updated, Version 4)
zr92e05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 683168 3'
                 Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 535;
               Score 27; DB 35; Length 441
Pred. No. 2.44e-02;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="germinal center B cell"
/lab_host="PalloB"
complement(<1..>535)
Sequence 535 BP; 153 A; 123 C; 101 G; 151 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 76; ]
Pred. No. 2.44e-02;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 aaaaaaaaaagacagtattttattgtaatatataa 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AAAAAAAAAGAAAGTATATTATTGTAAAAGATAA 258
                                                                                                                                                                                                                                                          .T 11
HSAA37572 standard; RNA; EST; 535 BP.
AA214564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%;
llarity 88.6%;
Conservative
               Query Match 5.8%;
Best Local Similarity 71.4%;
                                                     45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index";
Unpublished.
                                                                                                                                                               153 ttt 155
                                                                                                                                                                                                    TTT 224
```

NCI-CGAP;

226

RESULT ID HS AC AA NI 91 DT 031

Matches

셤 გ ្ន source

ö Gaps 'National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; ö Length 535; Indels 28-JUN-1997 (Rel. 52, Created) 28-JUN-1997 (Rel. 52, Last updated, Version 1) nh05c07.s1 NCI_CGAP_Thyl Homo sapiens cDNA clone 943404. Score 27; DB 14; Pred. No. 2.44e-02; NCI-CGAP;

10-JUN-1997

EST

mRNA

535 bp

AA214564

12

RESULT LOCUS

셤 ð

STITETT

source

ETTOCOCOCOCEETEEFEE

```
/clone_lib="NCI_CGAP_Thy1"
/tissue_type="thyroid"
/lab_host="DH10B"
<1..>154
                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amersham High quality sequence stop: 154.
Key Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                     4 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; RNA; EST; 200
                                                                                                                                          /clone="943404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 TCTTTTTTTTAATTTTT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 ttttttttttttttttt 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                           Query Match 5.6%;
Best Local Similarity 66.3%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                       O
                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repetitive element ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index";
                                                                                                                                                                                                                                                                     ĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JT 15
HSAA7745
AA507745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92244184
                                                                                                                                                                                                                          mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 - 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GSP clone distribution: NCI-GSP clone distribution information can be Gound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pAMP10; mRNA made from invasive thyroid tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 CGCTGGACTTTTTTCATTTTATATTTTGAATGGAGTATTATCTTTTACAATAATATACTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA493647 154 bp mRNA EST 26-JUN-1997
nh05c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone 943404.
AA493647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
Robert_Strausbergenih.gov Tissue Procurement: L. Jeffrey Medeiros,
M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation:
David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LinL at:
www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40ml3 fwd. ET
from Amersham High quality sequence stop: 83.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 83.
Location/Qualifiers
1..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 A; 15 C; 4 G; 126 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 67;
Pred. No. 1.00e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="943404"
/clone_lib="NCI_CGAP_Thy1"
/tissue_type="thyroid"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 ttttttttttttttttt 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 5.6%;
Local Similarity 66.3%;
Nes 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Gene Index";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 154 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92223488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

14

RESULT

235

S

g

28

ద c_D

Matches

mRNA

SEEES

DEFINITION

ACCESSION

URCE

KEYWORDS

NID

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

FEATURES

```
/note="vector: paMP10; mRNA made from invasive thyroid tumor, cDNA made by oligo-dr priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pAMP10; mRNA made from prostatic intraepithelial neoplasia (low-grade), cDNA made by oligo-dr priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) CancerResearch 56:5380-5383." /clone="941964"
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
Robert Strausbergenih.gov Tissue Procurement: David G. Bostwick,
M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kriaman, Ph.D. CDNA Library
Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington
University Genome Sequencing Center Clone distribution: NOT-CGAP
Clone distribution information can be found through the I.M.A.G.E.
Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert
Length: 473 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ಭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP;
"National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-1997 (Rel. 52, Created)
16-JUL-1997 (Rel. 52, Last updated, Version 2)
ng89c07.sl NCI_CGAP_Pr6 Homo sapiens cDNA clone 941964 similar
contains Alu repetitive element; contains element TAR1 TAR1
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                     Length 154;
                                                                                                                                                                                                                                                   Score 26; DB 32; Length 154
Pred. No. 1.00e-01;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 200 BP; 41 A; 54 C; 39 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="prostate"
/lab_host="DH10B"
<1...>200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
```

```
ó;
 Score 26; DB 80; Length 200;
Pred. No. 1.00e-01;
0; Mismatches 5; Indels 0; Gaps
Query Match
Best Local Similarity 86.1%;
Matches 31; Conservative
```

Op • g,

Search completed: Tue Feb 3 20:22:31 1998 Job time : 465 secs.

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

BLACK BORDERS

IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

FADED TEXT OR DRAWING

BLURRED OR ILLEGIBLE TEXT OR DRAWING

SKEWED/SLANTED IMAGES

COLOR OR BLACK AND WHITE PHOTOGRAPHS

GRAY SCALE DOCUMENTS

LINES OR MARKS ON ORIGINAL DOCUMENT

REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

IMAGES ARE BEST AVAILABLE COPY.

□ OTHER:

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.